

09:53:12 2004

us-10-063-557-50.rag

GenCore version 5.1.6
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in search, using sw model

unary 6, 2004, 15:59:10 : Search time 40 Seconds
(without alignments)
353.167 Million cell updates/sec

1-10-063-557-50

11

MERVTLALLLAGLTALEAN.....HSPVPEKAIPITPGSATTC 89

OSUM62

pop 10.0 , Gapext 0.5

07863 seqs, 158726573 residues

ts satisfying chosen parameters: 1107863

gth: 0

gth: 2000000000

inimum Match 0%

aximum Match 100%

isting first 45 summaries

Geneseq 19Jun03:*

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/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*

/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*

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/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
ad by analysis of the total score distribution.

SUMMARIES

seq	ch	Length	DB	ID	Description
0.0	89	21	AA1985679		Human kidney disea
0.0	89	21	AA1987258		Human signal pepti
0.0	89	21	AA1966705		Membrane-bound pro
0.0	89	22	AAU29123		Human PRO polyrept
0.0	89	22	AA197550		Human PRO1069, Ho
0.0	89	22	AA1965228		Human PRO1069 (UNQ
0.0	89	23	ABG95875		Human secreted/tra
0.0	89	24	ABU71211		Human PRO1069 prot
0.0	89	24	ABU71530		Human secreted pol

10	461	100.0	89	24	ABU71976	Novel hum
11	461	100.0	89	24	ABU72133	Human PRO
12	461	100.0	89	24	ABU65668	Human sec
13	461	100.0	89	24	ABU68001	Novel hum
14	461	100.0	89	24	ABU67505	Human sec
15	461	100.0	89	24	ABU65363	Human PRO
16	461	100.0	89	24	ABU59121	Novel hum
17	461	100.0	89	24	ABU59268	Human sec
18	461	100.0	89	24	ABU59417	Novel hum
19	461	100.0	89	24	ABU60552	Human sec
20	461	100.0	89	24	ABU58043	Human PRO
21	461	100.0	89	24	ABU58499	Human PRO
22	461	100.0	89	24	ABU58974	Human sec
23	461	100.0	89	24	ABU56035	Human sec
24	461	100.0	89	24	ABU57030	Human PRO
25	461	100.0	89	24	ABU13934	Human PRO
26	461	100.0	89	24	ABU10609	Human sec
27	461	100.0	89	24	ABU10889	Human PRO
28	452	98.0	89	20	AAW92958	Human zsi
29	452	98.0	89	22	AAW38770	Human pol
30	276.5	60.0	117	22	AAW40556	Human pol
31	276.5	60.0	88	22	AAE05362	Mouse cha
32	276.5	60.0	88	23	ABW72374	Marine pri
33	256.5	55.6	87	20	AAW92966	Rat CHIF j
34	241.5	52.4	88	17	AAW90991	Mouse Mat
35	214.5	46.5	87	17	AAW90990	Human Mat
36	214.5	46.5	87	20	AAW48304	Human PRO
37	214.5	46.5	87	20	AAW92959	Human MAT
38	214.5	46.5	87	22	AAW3962	Human EST
39	214.5	46.5	87	24	ABW47467	Breast cai
40	214.5	46.5	87	24	ABJ37036	Human brei
41	214.5	46.5	87	24	ABP75985	Human GEN
42	214.5	46.5	87	24	ABP76150	Human GEN
43	214.5	46.5	116	24	ABJ19334	NOVX relai
44	209.5	45.4	86	24	ABJ19333	NOVX relai
45	191.5	41.5	113	24	ABW47468	Breast cai

ALIGNMENTS

RESULT 1

AA1985679

ID AA1985679 standard; Protein; 89 AA.

AC AA1985679;

XX

XX

DT 13-FEB-2001 (first entry)

XX

DE Human kidney disease associated protein SEQ ID 11.

XX

Nephrotropic; cytostatic; human; kidney disease associated; hyper
Bartter's syndrome; Gitelman syndrome; nephrolithiasis; renal fai
renal amyloidosis; primary aldosteronism; Addison's disease; can
glomerulonephritis; dysplastic malformation; medullary cystic dis
medullary sponge kidney; tubular dysplasia; Alport's syndrome.

XX

OS Homo sapiens.

XX

PN W0200061622-A2.

XX

PD 19-OCT-2000.

XX

PF 28-MAR-2000; 2000WO-US08260.

XX

PR 09-APR-1999; 99US-0289349.

XX

PA (INCY-) INCYTE PHARM INC.

XX

PI Walker MG, Volkmut W, Klingler TM, Azimzai Y, Yue H;

XX

DR WPI; 2000-665116/64.

DR N-PSDB; AAC66135.

disease associated gene useful for diagnosing treating and renal disorders, is uromodulin, NKCC2, NCCT, aldolase B, H, PDZK1, NPT1, calbindin, kininogen or CIC-Kb -

re 35-36; 36pp; English.

des AAC66131-C66139 represent human kidney disease genes. Proteins AAY85678-Y85680 represent human kidney disease proteins. The polynucleotides have nephrotropic and cytostatic ie polynucleotides, encoded proteins and pharmaceutical containing them are useful for diagnosing, prognosis, preventing renal disorders such as Bartter's syndrome,ndrome, autosomal dominant polycystic kidney disease and is. The genes and proteins are also useful for identifying that are associated with a specific disease, regulatory cellular compartment, cell type, tissue type or species useful in diagnosis, prognosis, treatment and evaluation of renal diseases for e.g. renal amyloidosis, hypertension, steronism, Addison's disease, renal failure, Arthritis, chronic glomerulonephritis, tubulointerstitial ystic disorders and dysplastic malformations, inherited renal disease (PRD), medullary cystic disease, medullary y and tubular dysplasia. Alport's syndrome, non-renal they adenocarcinoma, metastatic renal carcinoma, multiple nephrotropic disorders.

9 AA;

100.0%; Score 461; DB 21; Length 89;
larity 100.0%; Pred. No. 1.2e-50;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

VTALLLLAGLTALEANDPFANKDDPFYDWKNLQSLGICGGLIATAGIAVLGSK 60
VTALLLLAGLTALEANDPFANKDDPFYDWKNLQSLGICGGLIATAGIAVLGSK 60
KSSQKQHSVPPEKAIPITPGSATTC 89
KSSQKQHSVPPEKAIPITPGSATTC 89

standard; Protein; 89 AA.

(first entry)

peptide containing protein HSP-35 SEQ ID NO:35.

1 peptide-containing protein; HSP; diagnosis; cancer;
; cardiovascular disease; anticancer; anti-inflammatory;
1; nontropic; neuroprotective; cardiovascular; hepatotropic;
c; gene therapy; cell proliferation; neurological disorder;
disorder; developmental disorder; arteriosclerosis;
soriasis; acquired immune deficiency syndrome; anaemia;
n's disease; infection; Alzheimer's disease; schizophrenia;
disease; Huntington's diseases; ovulatory defect;
trophy.

A2.

99WO-US14484.
98US-0090762.
98US-0094983.
98US-0102686.

11-DEC-1998; 98US-0112129.
(INCY-) INCYTE PHARM INC.
Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KU, Baughn I
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hill;
PI Bandman O;
XX
DR WPI; 2000-160E73/14.
DR N-PSDB; AAZ98143.
XX
XX
PT New human signal peptide-containing proteins useful in treatment
PT prevention and diagnosis of e.g. cancer, inflammation and
XX cardiovascular disease -
PS Claim 1; Page 182; 327pp; English.
XX
CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSP;
CC anticancer, anti-inflammatory, antimicrobial, nontropic, hepat
CC neuroprotective, cardiovascular and antiasthmatic activities, a
CC be used in gene therapy. HSPs can be used to treat or prevent c
CC associated with decreased activity or function of HSP. Antagon:
CC HSP are used to treat or prevent disorders associated with inc
CC activity or function of HSP. Such diseases include cell prolif
CC (including cancer), inflammation, cardiovascular, neurological
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anae
CC asthma, Crohn's disease, microbial or other infections, congest
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington'
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy).
CC nucleic acids can be used for the recombinant production of HSP
CC detecting HSP in standard hybridisation and amplification assa
CC diagnosis and monitoring), in gene therapy, as antisense,
CC triplex-forming or ribozyme therapeutics, for detecting related
CC or genetic variations, and for chromosomal mapping. HSP are als
CC raise specific antibodies (Ab) and to screen for agonists and
CC antagonists (potential therapeutic agents). Ab are used to diag
CC monitor, HSP-related diseases (in usual immunoassays) as ther
CC antagonists, in competitive drug screens, and for purification c
CC from natural sources.
XX
SQ Sequence 89 AA;

Query Match 100.0%; Score 461; DB 21; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e-50;
Matches 89; Conservative 0; Mismatches 0; Indels 0;

QY 1 MERVTLALLLLAGLTALEANDPFANKDDPFYDWKNLQSLGICGGLIATAGIAF
DB 1 MERVTLALLLLAGLTALEANDPFANKDDPFYDWKNLQSLGICGGLIATAGIAF
QY 61 CKYKSSQKQHSVPPEKAIPITPGSATTC 89
DB 61 CKYKSSQKQHSVPPEKAIPITPGSATTC 89

RESULT 3
AAY66705
ID AAY66705 standard; protein; 89 AA.
XX
AC AAY66705;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1069.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE 1
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS Homo sapiens.
XX
FN WO9963088-A2.

PR	25-JUN-1998;	98US-00906690
PR	25-JUN-1998;	98US-00906691
PR	25-JUN-1998;	98US-00906694
PR	25-JUN-1998;	98US-00906695
PR	25-JUN-1998;	98US-00906696
PR	26-JUN-1998;	98US-00908682
PR	26-JUN-1998;	98US-00908683
PR	01-JUL-1998;	98US-00913358
PR	01-JUL-1998;	98US-00913440
PR	02-JUL-1998;	98US-0091478
PR	02-JUL-1998;	98US-0091486
PR	02-JUL-1998;	98US-0091519
PR	02-JUL-1998;	98US-0091628
PR	02-JUL-1998;	98US-0091633
PR	02-JUL-1998;	98US-0091646
PR	02-JUL-1998;	98US-0091673
PR	07-JUL-1998;	98US-0091978
PR	09-JUL-1998;	98US-0091982
PR	10-JUL-1998;	98US-0092182
PR	20-JUL-1998;	98US-0093339
PR	30-JUL-1998;	98US-0094551
PR	04-AUG-1998;	98US-0095282
PR	04-AUG-1998;	98US-0095301
PR	04-AUG-1998;	98US-0095302
PR	04-AUG-1998;	98US-0095318
PR	04-AUG-1998;	98US-0095321
PR	10-AUG-1998;	98US-0095325
PR	10-AUG-1998;	98US-0095916
PR	10-AUG-1998;	98US-0095929
PR	10-AUG-1998;	98US-0096012
PR	11-AUG-1998;	98US-0096143
PR	12-AUG-1998;	98US-0096146
PR	17-AUG-1998;	98US-0096757
PR	17-AUG-1998;	98US-0096766
PR	17-AUG-1998;	98US-0096768
PR	17-AUG-1998;	98US-0096773
PR	17-AUG-1998;	98US-0096791
PR	17-AUG-1998;	98US-0096867
PR	17-AUG-1998;	98US-0096891
PR	17-AUG-1998;	98US-0096894
PR	17-AUG-1998;	98US-0096895
PR	17-AUG-1998;	98US-0096897
PR	18-AUG-1998;	98US-0096949
PR	18-AUG-1998;	98US-0096950
PR	18-AUG-1998;	98US-0096956
PR	18-AUG-1998;	98US-0096960
PR	19-AUG-1998;	98US-0097022
PR	20-AUG-1998;	98US-0097141
PR	24-AUG-1998;	98US-0097218
PR	26-AUG-1998;	98US-0097661
PR	26-AUG-1998;	98US-0097951
PR	26-AUG-1998;	98US-0097952
PR	26-AUG-1998;	98US-0097954
PR	26-AUG-1998;	98US-0097955
PR	26-AUG-1998;	98US-0097971
PR	26-AUG-1998;	98US-0097974
PR	26-AUG-1998;	98US-0097978
PR	26-AUG-1998;	98US-0097979
PR	26-AUG-1998;	98US-0097986
PR	31-AUG-1998;	98US-0098014
PR	16-SEP-1998;	98US-0098525
PR	12-JAN-1999;	98US-0100634
XX		99US-0115565
PA	(GETH) GEMENTECH INC.	
XX		
PI	Baker K, Chen J, Goddard A,	
PI	Wood WI, Yuan J;	

Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK; Wood WI, Yuan J;

'2883/06.
15045.

and proteins and related nucleotide sequences -

9 180; 822pp; English.

in provides membrane-bound PRO polypeptides and des encoding them. The PRO sequences of the invention were based on extracellular domain homology screening. The PRO ve homology with proteins including LDL receptors, TIE various enzymes. The membrane-bound proteins and receptor e useful as pharmaceutical and diagnostic agents. Receptor ns, for instance, can be used as therapeutic agents to block and interactions. The membrane-bound proteins can also be screening of potential peptide or small molecule inhibitors ant receptor/ligand interaction. The PRO encoding inhibitors s hybridization probes, in chromosome and gene mapping and in on of antisense RNA and DNA. PRO nucleic acid sequences useful for the preparation of PRO polypeptides, especially nt techniques.

9 AA;

100.0%; Score 461; DB 21; Length 89;
larity 100.0%; Pred. No. 1.2e-50;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

VTLALLLAGLTALEANDPFANKDDPFYDWNKQLSLGICGGLAAGIAVLGSK 60
|||||
VTLALLLAGLTALEANDPFANKDDPFYDWNKQLSLGICGGLAAGIAVLGSK 60

KSSQKQHSVPPEKAIPITPGSATTC 89
|||||
KSSQKQHSVPPEKAIPITPGSATTC 89

ndard; Protein; 89 AA.

(first entry)

lypeptide sequence #100.

ide; mammal; tumour; cancer; human; cattle; horse; sheep;
3; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
rocyte cell; cell proliferation; cell differentiation; colon;
3; breast; prostate; rectum; cervix; liver; genetic disorder.

42.

2001WO-US06520.

2000WO-US05601.
2000WO-US05841.
2000US-187202P.
2000US-186968P.
2000US-189320P.
2000US-189328P.
2000WO-US06884.
2000US-190828P.
2000US-191007P.
2000US-191048P.
2000US-191314P.
2000US-192655P.

29-MAR-2000; 2000US-191032P.
PR 29-MAR-2000; 2000US-191053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-064848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurr
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2001-602746/68.
N-PSDB; AAS46024.

Novel nucleic acids encoding PRO polypeptides, used to diagnose
presence of tumours, such as prostate and breast tumours, in man
to screen for modulators of the compounds -

Claim 11; Fig 200; 774pp; English.

Sequences AAU2924-AU29328 represent PRO polypeptides of the in
The PRO polypeptides and their associated nucleic acids can be u
detect the presence of a tumour in a mammal by comparing the lev
expression of a PRO polypeptide in a test sample of cells from t
and a control sample of normal cells, whereby a higher level of
expression in the test sample indicates the presence of a tumour
mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs,
and rabbits but are preferably human. The polypeptides can be us
stimulate tumour necrosis factor (TNF) alpha release from human
when contacted with it. A specific polypeptide can be used to st
the proliferation or differentiation of chondrocyte cells. The p
proteins can be used to determine the presence of tumours and al
susceptibility to tumour development, particularly adrenal, lung
breast, prostate, rectal, cervical, or liver tumours, in mammali
subjects. The oligonucleotide probes specific for the PRO nuclei
can be used for genetic analysis of individuals with genetic dis

Sequence 89 AA;

Query Match 100.0%; Score 461; DB 22; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e-50;
Matches 89; Conservative 0; Mismatches 0; Indels 0; (

QY 1 MERVTLALLLAGLTALEANDPFANKDDPFYDWNKQLSLGICGGLAAGIAA'
Db 1 MERVTLALLLAGLTALEANDPFANKDDPFYDWNKQLSLGICGGLAAGIAA'
QY 61 CKYKSSQKQHSVPPEKAIPITPGSATTC 89
Db 61 CKYKSSQKQHSVPPEKAIPITPGSATTC 89

ard; Protein; 89 AA.

(first entry)

rotein; mapping.

2.

2000WO-US23328.

99WO-US20111.
99WO-US21090.
99US-0169495.
99US-0170262.
2000US-0175481.
2000WO-US04341.
2000WO-US04342.
2000WO-US04414.
2000WO-US05601.
2000US-0187202.
2000US-0193397.
2000WO-US14042.
2000US-0209832.

TECH INC.

Ivaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Gurney AL, Watanabe CK, Wood WI;

260/18.
382.

ucleic acids encoding PRO polypeptides, useful in
logy, including use as hybridization probes, and in
i gene mapping. -

50; 278pp; English.

sequence is a human PRO polypeptide (secreted and
). The PRO protein, and PRO agonists, PRO antagonists or
odies are useful for preparation of a medicament useful in
of a condition which is responsive to the PRO protein,
agonists or anti-PRO antibodies. The PRO protein may also be
lecular weight markers for protein electrophoresis. The PRO
e has applications in molecular biology, including use as
probes, and in chromosome and gene mapping.

AA;

arity 100.0%; Score 461; DB 22; Length 89;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

TLALLLAGLTALEANDPFANKDDPFYDWNKQLSLGGLIAGIAVLGSK 60
TLALLLAGLTALEANDPFANKDDPFYDWNKQLSLGGLIAGIAVLGSK 60
SSQKQHSVPVPEKAIPILITPGSATTC 89
SSQKQHSVPVPEKAIPILITPGSATTC 89

RESULT 6
AAB65228
ID AAB65228 standard; Protein; 89 AA.
XX
AC AAB65228;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1069 (JNQ526) protein sequence SEQ ID NO:262.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue tyf
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO2000073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US08439.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 26-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 18-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AU, Baker KP, Botstein D, Desnovers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godows
PI Grimaldi CJ, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni
PI Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM, Wood
PI Zhang Z;
XX
DR WPI; 2001-032160/04.
DR N-PSDB; AAF44191.
XX
PT PRO polynucleotides used to produce polypeptides used to target
PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -
XX
PS Claim 12; Fig 180; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane
CC proteins. The PRO proteins have cytostatic activity. The PRO prot
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nuc
CC sequences, and their fragments, can be used as hybridisation prob
CC chromosomal and gene mapping, and in the generation of anti-sense
CC and DNA. They may also be used to produce transgenic animals whic
CC used to develop and screen therapeutically useful reagents. The P
CC nucleotide and protein sequence can be used for tissue typing and

PR 21-NOV-1997; 97US-066120P.
PR 24-NOV-1997; 97US-066466P.
PR 24-NOV-1997; 97US-066772P.
PR 11-DEC-1997; 97US-069335P.
PR 12-DEC-1997; 97US-069425P.
PR 17-DEC-1997; 97US-069870P.
PR 18-DEC-1997; 97US-068017P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077649P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078939P.
PR 27-MAR-1998; 98US-079664P.
PR 31-MAR-1998; 98US-079786P.
PR 31-MAR-1998; 98US-080107P.
PR 31-MAR-1998; 98US-080194P.
PR 01-APR-1998; 98US-080327P.
PR 01-APR-1998; 98US-080333P.
PR 08-APR-1998; 98US-081049P.
PR 08-APR-1998; 98US-081070P.
PR 09-APR-1998; 98US-081195P.
PR 15-APR-1998; 98US-081838P.
PR 21-APR-1998; 98US-082568P.
PR 21-APR-1998; 98US-082569P.
PR 22-APR-1998; 98US-082704P.
PR 22-APR-1998; 98US-082797P.
PR 28-APR-1998; 98US-083322P.
PR 29-APR-1998; 98US-083495P.
PR 29-APR-1998; 98US-083496P.
PR 29-APR-1998; 98US-083499P.
PR 29-APR-1998; 98US-083559P.
PR 05-MAY-1998; 98US-084366P.
PR 06-MAY-1998; 98US-084414P.
PR 07-MAY-1998; 98US-084639P.
PR 07-MAY-1998; 98US-084640P.
PR 07-MAY-1998; 98US-084643P.
PR 15-MAY-1998; 98US-085579P.
PR 15-MAY-1998; 98US-085580P.
PR 15-MAY-1998; 98US-085582P.
PR 15-MAY-1998; 98US-085700P.
PR 18-MAY-1998; 98US-086023P.
PR 22-MAY-1998; 98US-086392P.
PR 22-MAY-1998; 98US-086486P.
PR 28-MAY-1998; 98US-087098P.
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PR 02-JUN-1998; 98US-087609P.
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PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088025P.
PR 04-JUN-1998; 98US-088028P.
PR 04-JUN-1998; 98US-088029P.
PR 04-JUN-1998; 98US-088033P.
PR 04-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.
PR 05-JUN-1998; 98US-088217P.
PR 09-JUN-1998; 98US-088655P.
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PR 10-JUN-1998; 98US-088738P.
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PR 10-JUN-1998; 98US-088826P.
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PR 12-JUN-1998; 98US-089090P.
PR 12-JUN-1998; 98US-089105P.
PR 15-JUN-1998; 98US-089512P.
PR 16-JUN-1998; 98US-089514P.
PR 17-JUN-1998; 98US-089538P.

dard; Protein; 89 AA.

(first entry)
protein.
ecrated; transmembrane; cytostatic; TNF-alpha; blood;
is factor alpha release; chondrocyte cell; proliferation;
on; tumour; Gene therapy.

A1.

2002US-0187600.
98WO-US19330.
98WO-US21141.
98WO-US25108.
99WO-US05028.
99WO-US10733.
99WO-US12252.
99WO-US20111.
99WO-US21090.
99WO-US28301.
99WO-US28551.
99WO-US31274.
2000WO-US00219.
2000WO-US04341.
2000WO-US04342.
2000WO-US04414.
2000WO-US05004.
2000WO-US05601.
2000WO-US05841.
2000WO-US06884.
2000WO-US08439.
2000WO-US13705.
2000WO-US14042.
2000WO-US14941.
2000WO-US15264.
2000WO-US20710.
2000WO-US23328.
2000WO-US30952.
2000WO-US32678.
2000WO-US34956.
2001WO-US06520.
2001WO-US17800.
2001WO-US19692.
2001WO-US21066.
2001WO-US21735.
2001WO-US27099.
97US-059263P.
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97US-063870P.
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 98US-098843P.
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 98US-099741P.
 98US-099754P.
 98US-099763P.
 98US-099812P.

arity 100.0%; Score 461; DB 24; Length 89;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;

TTIALLLAGLTALEANDPFYVDWKNLQSLGICGGLLAIAAGIAVLGSK 60
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TTIALLLAGLTALEANDPFYVDWKNLQSLGICGGLLAIAAGIAVLGSK 60
 |||||

SSQKHSPVPEKAIPLITPGSATTC 89

SSQKHSPVPEKAIPLITPGSATTC 89

ABU71530
 ID ABU71530 standard; Protein; 89 AA.
 XX
 AC ABU71530;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Human secreted polypeptide PRO1069.
 XX
 KW Human; gene therapy; tumour; cancer.
 XX
 OS Homo sapiens.
 XX
 FN US2003013855-A1.
 XX
 PD 16-JAN-2003.
 XX
 PF 03-MAY-2002; 2002US-0063616.
 XX
 PR 30-DEC-1998; 98KR-0062142.
 PR 08-MAR-1999; 99WO-US05028.
 PR 14-MAY-1999; 99WO-US10733.
 PR 30-DEC-1999; 99WO-US31274.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 02-JUN-2000; 2000WO-US14042.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 14-MAY-1999; 99US-0311832.
 PR 25-AUG-1999; 99US-0380137.
 PR 25-AUG-1999; 99US-0380138.
 PR 25-AUG-1999; 99US-0380139.
 PR 15-SEP-1999; 99US-0380142.
 PR 18-OCT-1999; 99US-0403297.
 PR 12-NOV-1999; 99US-0423844.
 PR 22-AUG-2000; 2000US-0644844.
 PR 18-SEP-2000; 2000US-0664610.
 PR 08-NOV-2000; 2000US-0709238.
 PR 20-DEC-2000; 2000US-0747259.
 PR 22-MAR-2001; 2001US-0816744.
 PR 10-MAY-2001; 2001US-0854208.
 PR 30-MAY-2001; 2001US-0870574.
 PR 05-JUN-2001; 2001US-0874503.
 PR 29-JUN-2001; 2001US-0869599.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-DEC-2001; 2001US-0006867.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 DR WPI; 2003-330485/31.
 DR N-PSDB; ACA58834.
 XX
 PT New isolated antibody specifically binding a PRO polypeptide, use
 PT for the preparation of a medicament for treating disorders with t
 PT aberrant expression or activity of the PRO polypeptide, such as t
 XX conditions and cancer -
 PS Disclosure; Page 117; 406pp; English.
 XX
 CC The invention relates to an antibody that binds to a polypeptide

sequence given in the specification. The methods and (containing antibodies that specifically bind a PRO of the present invention are useful for the preparation of a treatment of disorders associated with the aberrant activity of the PRO polypeptide, such as tumour conditions they can also be used to generate transgenic or knockout PRO polypeptides and screening of therapeutically useful PRO polypeptides and encoding nucleic acids can be used as markers for protein electrophoresis, chromosome and tissue typing. The PRO polypeptides are useful to enesis e.g wound healing; in the treatment of sports-related, articular cartilage defects, osteoarthritis or rheumatoid abetes; hyperinsulinaemia and hypoinsulinaemia. The y be used in various diagnostic, competitive binding and/or tation assays. The present sequence represents the amino of a PRO polypeptide of the invention.

AA;

100.0%; Score 461; DB 24; Length 89;
arity 100.0%; Pred. No. 1.2e-50;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

TLALLLAGLTALEANDPFANKDPPFYDWKNLQSLICGGLIAIAGIAVLSGK 60
TLALLLAGLTALEANDPFANKDPPFYDWKNLQSLICGGLIAIAGIAVLSGK 60

SSQKQHSVPVEKAIPITPGSATTC 89
|||||
SSQKQHSVPVEKAIPITPGSATTC 89

lard; Protein; 89 AA.

(first entry)

creted and transmembrane protein PRO1069.

ed and transmembrane polypeptide;
oping; gene mapping; transgenic animal; knockout animal;
fent screening; chromosome identification; tissue typing;

11.

002US-0063512.

001US-0006867.

TECH INC.

varoff E, Gerritsen ME, Goddard A, Godowski PJ;
Gurney AL, Watanabe CK, Wood WI;

084/31.
087.

und transmembrane PRO polypeptides and nucleic acid
ding the polypeptides, useful in gene therapy or
dicament for treating a condition that is responsive to
ptide or antibody -

g 50; 409pp; English.

describes novel isolated PRO polypeptides. The PRO

polypeptides or anti-PRO antibodies are useful in preparing a me for treating a condition that is responsive to the PRO polypepti antibody. The PRO nucleotide sequences may be used as hybridisat probes in chromosome and gene mapping, or in generating antisens CC and DNA. PRO nucleic acids are also useful in preparing PRO poly CC in assays to identify other proteins or molecules involved in bi CC reaction, to generate transgenic animals or knockout animals, wh CC turn are useful in the development and screening of therapeutica CC useful reagents, for chromosome identification, and tissue typin CC PRO polypeptides and nucleic acid molecules are also useful in g CC therapy, and as molecular weight markers for protein electrophor CC purposes. The anti-PRO antibodies may be used in diagnostic assa CC PRO, or for the affinity purification of PRO from recombinant ce CC culture or natural sources. This is the amino acid sequence of a CC human secreted and transmembrane PRO polypeptide.

XX Sequence 89 AA;

Query Match 100.0%; Score 461; DB 24; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e-50;
Matches 89; Conservative 0; Mismatches 0; Indels 0; (

QY 1 NERVTLALLLAGLTALEANDPFANKDPPFYDWKNLQSLICGGLIAIAGIAA
Db 1 NERVTLALLLAGLTALEANDPFANKDPPFYDWKNLQSLICGGLIAIAGIAA

QY 61 CKYKSSQKQHSVPVEKAIPITPGSATTC 89
|||||

Db 61 CKYKSSQKQHSVPVEKAIPITPGSATTC 89
|||||

RESULT 11

ABU72133
ID ABU72133 standard; Protein; 89 AA.

XX AC ABU72133;

DT 13-JUN-2003 (first entry)

DE Human PRO polypeptide #25.

XX Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression.

XX Homo sapiens.

XX US2003023042-A1.

XX 30-JAN-2003.

XX 01-MAY-2002; 2002US-0063502.

XX 06-DEC-2001; 2001US-0006867.

XX (GETH) GENENTECH INC.

XX Eaton DL, Pilvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

XX WPI; 2003-331484/31.

XX DR N-PSDB; ACA63397.

XX Novel monoclonal antibody that binds to secreted and transmembran
PT polypeptide, useful for detecting and purifying the polypeptide a
PT also for treating conditions responsive to the antibody -
XX Disclosure; Fig 50; 408pp; English.

XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a
CC medicament useful in the treatment of a condition responsive to

ibody. Anti-PRO antibodies are useful in diagnostic
PRO, by detecting its expression in specific cells,
serum, and for affinity purification of PRO from
cell culture or natural sources. ABU72109-ABU72192
are human PRO polypeptides of the invention.

39 AA;

100.0%; Score 461; DB 24; Length 89;

ilarity 100.0%; Pred. No. 1.2e-50;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RYTALLLLAGLTALANDPFANKDDPFYDWNKQLSLGGLIAGIAIAVLGSK 60

RYTALLLLAGLTALANDPFANKDDPFYDWNKQLSLGGLIAGIAIAVLGSK 60

KSSQKHSPVPEKAIPITPGSATTC 89

KSSQKHSPVPEKAIPITPGSATTC 89

ndard; Protein; 89 AA.

(first entry)

ed/transmembrane protein, SEQ ID 200.

secreted protein; transmembrane protein;
antiarthritic; osteopathic; adrenal tumour; lung tumour;
; breast tumour; prostate tumour; rectal tumour;
our; liver tumour; TNF-alpha release; arthritis;
sis factor alpha; chondrocyte cell; bone disorder;
sorder; sports injury.

-Al.

2002US-0188767.

98WO-US19330.

98WO-US21141.

98WO-US25108.

99WO-US05028.

99WO-US10733.

99WO-US12252.

99WO-US20111.

99WO-US21090.

99WO-US28101.

99WO-US31274.

2000WO-US00219.

2000WO-US04341.

2000WO-US04342.

2000WO-US04414.

2000WO-US05004.

2000WO-US05601.

2000WO-US05841.

2000WO-US06884.

2000WO-US08439.

2000WO-US13705.

2000WO-US14042.

2000WO-US14941.

2000WO-US15264.

2000WO-US20710.

2000WO-US23328.

2000WO-US30952.

01-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US34956.
28-FEB-2001; 2001WO-US06520.
01-JUN-2001; 2001WO-US17800.
20-JUN-2001; 2001WO-US19692.
29-JUN-2001; 2001WO-US21066.
09-JUL-2001; 2001WO-US21735.
29-AUG-2001; 2001WO-US27099.
18-SEP-1997; 97US-059263P.
18-SEP-1997; 97US-059268P.
17-OCT-1997; 97US-062250P.
21-OCT-1997; 97US-063486P.
24-OCT-1997; 97US-063120P.
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31-OCT-1997; 97US-063870P.
31-OCT-1997; 97US-064103P.
13-NOV-1997; 97US-065311P.
21-NOV-1997; 97US-066120P.
24-NOV-1997; 97US-066466P.
11-DEC-1997; 97US-066772P.
12-DEC-1997; 97US-069335P.
17-DEC-1997; 97US-069435P.
18-DEC-1997; 97US-069870P.
10-MAR-1998; 97US-068017P.
11-MAR-1998; 97US-077450P.
11-MAR-1998; 98US-077632P.
20-MAR-1998; 98US-077649P.
20-MAR-1998; 98US-078886P.
20-MAR-1998; 98US-078939P.
27-MAR-1998; 98US-079684P.
27-MAR-1998; 98US-079786P.
31-MAR-1998; 98US-080107P.
31-MAR-1998; 98US-080194P.
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01-APR-1998; 98US-080333P.
08-APR-1998; 98US-081049P.
08-APR-1998; 98US-081070P.
09-APR-1998; 98US-081195P.
15-APR-1998; 98US-081838P.
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21-APR-1998; 98US-082569P.
22-APR-1998; 98US-082704P.
22-APR-1998; 98US-082797P.
28-APR-1998; 98US-083322P.
29-APR-1998; 98US-083495P.
29-APR-1998; 98US-083496P.
29-APR-1998; 98US-083499P.
29-APR-1998; 98US-083559P.
05-MAY-1998; 98US-084366P.
06-MAY-1998; 98US-084414P.
07-MAY-1998; 98US-084639P.
07-MAY-1998; 98US-084640P.
07-MAY-1998; 98US-084643P.
15-MAY-1998; 98US-085579P.
15-MAY-1998; 98US-085580P.
15-MAY-1998; 98US-085582P.
15-MAY-1998; 98US-085700P.
18-MAY-1998; 98US-086023P.
22-MAY-1998; 98US-086392P.
22-MAY-1998; 98US-086486P.
28-MAY-1998; 98US-087098P.
28-MAY-1998; 98US-087208P.
02-JUN-1998; 98US-087609P.
02-JUN-1998; 98US-087759P.
03-JUN-1998; 98US-087827P.
04-JUN-1998; 98US-088025P.
04-JUN-1998; 98US-088029P.
04-JUN-1998; 98US-088029P.

98US-088033P.
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 98US-098803P.

PR 02-SEP-1998; 98US-098821P.
 PR 02-SEP-1998; 98US-098843P.
 PR 09-SEP-1998; 98US-099602P.
 PR 10-SEP-1998; 98US-099741P.

Query Match 100.0%; Score 461; DB 24; Length 89;
 Best Local Similarity 100.0%; Pred. No. 1.2e-50;
 Matches 89; Conservative 0; Mismatches 0; Indels 0;

QY 1 MERVTLALLLAGLTALEANDPFANKDDPFYDWNKLNQISGLICGLLAIAIAA
 Db 1 MERVTLALLLAGLTALEANDPFANKDDPFYDWNKLNQISGLICGLLAIAIAA
 QY 61 CKYKSSQKQHSVPPEKAIPITPGSATTC 89
 Db 61 CKYKSSQKQHSVPPEKAIPITPGSATTC 89

RESULT 13

ABU66001
 ID ABU66001 standard; Protein; 89 AA.
 XX AC ABU66001;
 XX DT 20-MAY-2003 (first entry)
 XX DE Novel human secreted and transmembrane protein PRO1069.
 KW Human; secreted protein; transmembrane protein; cytostatic;
 KW Gene therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour;
 KW adrenal tumour; lung tumour; colon tumour; breast tumour;
 KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
 XX OS Homo sapiens.
 XX PN US2003036157-A1.
 XX PD 20-FEB-2003.
 XX PF 02-JUL-2002; 2002US-0188769.
 XX PR 16-SEP-1998; 98WO-US19330.
 PR 07-OCT-1998; 98WO-US21141.
 PR 01-DEC-1998; 98WO-US25108.
 PR 08-MAR-1999; 99WO-US05028.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 13-SEP-1999; 99WO-US21090.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28551.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
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 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.

2001WO-US21066.
2001WO-US21735.
2001WO-US27099.
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09:53:12 2004

us-10-063-557-50.rag

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(first entry)

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04-SEP-2001; 2001US-0946374.
15-JAN-2002; 2002US-0052586.

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurne
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-332039/31.
N-PSDB; ACA05799.

New secreted and transmembrane PRO polypeptides and nucleic acids
useful in gene therapy, in chromosome and gene mapping, as chromo
markers, in tissue typing, and in chromosome identification -

Claim 11; Fig 200; 706pp; English.

The invention discloses human nucleic acids encoding secreted and
transmembrane (PRO) polypeptides. Also disclosed is an antibody t
specifically binds to the PRO polypeptide, a method for stimulat
release of tumour necrosis factor alpha (TNF-alpha) from human bl
contacting the blood a PRO polypeptide, a method for stimulating
proliferation or differentiation of chondrocyte cells by contacti
cells with a PRO polypeptide, a method for detecting the presence
tumour in a mammal and an oligonucleotide probe derived from any
PRO nucleotide sequences. The nucleotide sequences are useful as
in chromosome and gene mapping, in generating antisense RNA and D
preparing PRO polypeptides by recombinant techniques and in gene
(e.g. for replacement of defective gene). The PRO polypeptides ar
as molecular weight markers for protein electrophoresis purposes,
chromosome identification, as chromosome markers, as therapeutic
for stimulating the release of TNF-alpha from human blood, for
stimulating the proliferation or differentiation of chondrocytes
detecting the presence of a tumour. The PRO polypeptides and nucl
acids may also be used diagnostically for tissue typing. The sequ
presented in ABU67406-ABU67710 are the PRO polypeptides of the in

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(first entry)

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1.0	88	4	US-09-724-864-58	Sequence 58, Appl
1.6	87	1	US-08-725-531-5	Sequence 5, Appl
1.6	87	2	US-08-738-127-5	Sequence 5, Appl
1.6	87	2	US-09-213-392-5	Sequence 5, Appl
1.6	87	2	US-09-083-661-5	Sequence 5, Appl
1.5	87	1	US-08-289-247B-4	Sequence 4, Appl
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1.4	120	4	US-09-996-243-199	Sequence 199, App
1.0	69	4	US-09-149-476-606	Sequence 606, App
1.6	72	3	US-08-905-223-405	Sequence 405, App
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; APPLICANT: Walker, Michael, G.
; APPLICANT: Volkuth, Wayne
; APPLICANT: Klinger, Ted, M.
; APPLICANT: Azimzai, Yalda
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: GENES ASSOCIATED WITH DISEASES OF THE KIDNEY
; FILE REFERENCE: PB-0010 US
; CURRENT APPLICATION NUMBER: US/09/289,349
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 12
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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critsen, Mary E.
idard, Audrey
owski, Paul J.
imaldi, J. Christopher
ney, Austin L.
javin, Ivar J.
pier, Mary A.
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ni, Nicholas F.
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ewart, Timothy A.
was, Daniel
tanabe, Colin K.
lliams, P. Mackey
od, William I.
ang, Zemin
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472

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ON NUMBER: 60/091982
TE: 1998-07-07
ON NUMBER: 60/092182
TE: 1998-07-09

100.0%; Score 461; DB 4; Length 89;
arity 100.0%; Pred. No. 8.5e-52;
onservative 0; Mismatches 0; Indels 0; Gaps 0;

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SSQKQHSVPVEKAIPITPGSATTC 89
|||
SSQKQHSVPVEKAIPITPGSATTC 89

lication US/09724864

62

ION:

son, James D.
son, James G.

ION: Polynucleotides, polypeptides expressed

ION: by the polynucleotides and methods for their use.

11000.105003

TION NUMBER: US/09/724,864

DATE: 2000-11-28

ON NUMBER: U.S. No. 6380362 60/171,678

TE: 1999-12-23

D NOS: 72

SEQ for Windows Version 4.0

; SEQ ID NO 58
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-58

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Matches 60; Conservative 8; Mismatches 19; Indels 3;
QY 1 MERVTLA-LLLLAGLTALANDPFANKDPPFYDKNLQSLGICGGLLAIAGIAA
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Db 1 MERVTLA-LLLLAGLTALANDPFANKDPPFYDKNLQSLGICGGLLAIAGIAA
|||
QY 60 KCKYKSSQKQHSVPVEKAIPITPGSATTC 89
|||
Db 60 KCKCRTHKP-SSLPGKATPLIIFGSANTC 88

RESULT 4

US-08-725-531-5
; Sequence 5, Application US/08725531
; Patent No. 5756310
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLENMAN-LIKE PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,531
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0128 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 951423
US-08-725-531-5

Query Match
Best Local Similarity 55.6%; Score 256.5; DB 1; Length 87;
Matches 56; Conservative 11; Mismatches 17; Indels 7; G
QY 1 MERVTLA-LLLLAGLTALANDPFANKDPPFYDKNLQSLGICGGLLAIAGIAA
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Db 1 MERVTLA-LLLLAGLTALANDPFANKDPPFYDKNLQSLGICGGLLAIAGIAA
|||

SEQUENCE CHARACTERISTICS:
LENGTH: 87
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-289-247B-4

Query Match 46.5%; Score 214.5; DB 1; Length 87;
Best Local Similarity 54.5%; Pred. No. 3.8e-20;
Matches 48; Conservative 11; Mismatches 24; Indels 5;

QY 1 MERVTLALLL-LAGLTALEANDPFANKDDPFYDWNKLNLSGLICGGLIAAGIA
Db 1 MOKVTLGLLVFLAGFPVLDAND-LEDKNSPFYDWNHSLQVGLICAGVLCAMGII
QY 60 KCKYKSSQKQ-HSPVPEKAIPLTIPGSA 86
Db 60 KCKKFGQKSGHH--PGETPPLITPGSA 85

RESULT 9

US-08-725-531-4

Sequence 4, Application US/08725531
Patent No. 5756310
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSES: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725.531
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0128 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1085026
US-08-725-531-4

Query Match 46.5%; Score 214.5; DB 1; Length 87;
Best Local Similarity 54.5%; Pred. No. 3.8e-20;
Matches 48; Conservative 11; Mismatches 24; Indels 5;

QY 1 MERVTLALLL-LAGLTALEANDPFANKDDPFYDWNKLNLSGLICGGLIAAGIA
Db 1 MOKVTLGLLVFLAGFPVLDAND-LEDKNSPFYDWNHSLQVGLICAGVLCAMGII

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Similarity 61.5%; Pred. No. 1.5e-25;
Conservative 11; Mismatches 17; Indels 7; Gaps 4;
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TCAFLVLVLAGLPVLEANGP-VDKSGPFYDWNHSLQVGLICAGVLCAMGII 59
KSSQKQHSP-VPEKAIPLTIPGSA 88
---CRNHTPSSLPEKVTPLITPGSAST 87

Location US/08289247B

ATTORNEY:
Morrisson, Briggs W.
Feder, Philip
INVENTION: Detection and Treatment of Breast
CANCER
REFERENCES: 4
ADDRESS:
Clark & Elbing LLP
16 Federal Street
Boston
Massachusetts
U.S.A.
1-2223

FILE FORM:
3.5" Diskette, 1.44 Mb
IBM PS/2 Model 50Z or 55SX
SYSTEM: MS-DOCS (Version 5.0)
WordPerfect (Version 5.1)
APPLICATION DATA:
NUMBER: US/08/289,247B
August 11, 1994
INFORMATION:
NUMBER:
INFORMATION:
ter-Brady, Kristina
NUMBER: 39,109
DOCKET NUMBER: 00383/021001
INFORMATION:
(617) 428-0200
(617) 428-7045

SEQ ID NO: 4

YKSSQKQ-HSPVPEKAIPITPGSA 86
 CKFGQKSGHH--PGETPPLITPGSA 85

lication US/08738127

655

ATION:

Bandman, Olga

Hawkins, Phillip R.

ENTION: NOVEL HUMAN PHOSPHOLEMMAN HOMOLOG

QUENCES: 6

CE ADDRESS:

Incyte Pharmaceuticals, Inc.

174 Porter Drive

o Alto

US

4

DABLE FORM:

E: Diskette

IBM Compatible

SYSTEM: DOS

FastSEQ Version 1.5

ICATION DATA:

N NUMBER: US/08/738,127

E: Filed Herewith

ATION DATA:

N NUMBER:

E:

NT INFORMATION:

lings, Lucy J.

ON NUMBER: 36,749

DOCKET NUMBER: PF-0141 US

ATION INFORMATION:

415-855-0555

415-845-4166

R SEQ ID NO: 4:

RACTERISTICS:

7 amino acids

no acid

SS: single

linear

E: peptide

URCE:

GenBank

85026

46.5%; Score 214.5; DB 2; Length 87;
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YKSSQKQ-HSPVPEKAIPITPGSA 86

CKFGQKSGHH--PGETPPLITPGSA 85

lication US/09213392

505

ATION:

Bandman, Olga

Goli, Surya K.

ENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN

NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/213,392

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/083,661

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0128 US

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 87 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 1085026

US-09-213-392-4

Query Match 46.5%; Score 214.5; DB 2; Length 87;
 Best Local Similarity 54.5%; Pred. No. 3.8e-20;
 Matches 48; Conservative 11; Mismatches 24; Indels 5;

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Db 1 MQKVTLLGLLVFLAGFPVLDAND-LEDKNSPFYYDWHLSLQVGLGGLICAGVLCAMGII

Qy 60 KCKYKSSQKQ-HSPVPEKAIPITPGSA 86

Db 60 KCKKFGQKSGHH--PGETPPLITPGSA 85

RESULT 12

US-09-083-661-4

Sequence 4, Application US/09083661

Patent No. 5955283

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Goli, Surya K.

TITLE OF INVENTION: NOVEL HUMAN PHOSPHOLEMMAN-LIKE PROTEIN

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

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: T INFORMATION:
: ings, Lucy J:
: N NUMBER: 36,749
: CCKET NUMBER: PF-0128 US
: TION INFORMATION:
: 415-855-0555
: 15-845-4166
: SEQ ID NO: 4:
: ACTERISTICS:
: amino acids
: o acid
: S: single
: linear
: : peptide
: RCE:
: enBank
: 5026

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46.5%; Score 214.5; DB 2; Length 87;
arity 54.5%; Pred. No. 3.8e-20;
onservative 11; Mismatches 24; Indels

[illegible]

ication US/08738127

55
TION: andman, Olga
awkins, Phillip R.
ENTION: NOVEL HUMAN PHOSPHOLEMMAN HOMOLOG
UNCES: 6
E ADDRESS: Incyte Pharmaceuticals, Inc.
74 Porter Drive
Alto

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IBM Compatible
SYSTEM: DOS
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N NUMBER: 36,749
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5-845-4166
SEQ ID NO: 1:
ACTERISTICS:

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; LENGTH: 92 amino acids
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; TOPOLOGY: linear
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Db	73	PDE 75 :			

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; Sequence 120, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouqueloret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 120
; LENGTH: 92
; TYPE: prt
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20...-1
US-09-247-155-120

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Best Local Similarity 41.3%; Pred. NO. 4e-09;
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74 PEK 76
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Db     73 PDE 75
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RESULT 15
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; Sequence 3, Application US/08725531
; Patent No. 5756310
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga

27.4%; Score 126.5; DB 1; Length 92;
larity 41.4%; Pred.No.8.4e-09;
Conservative 15; Mismatches 23; Indels 3; Gaps 2;

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HSPVPEK 76
: | :
RTGEDE 75

January 6, 2004, 16:05:14

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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gth: 0

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0.0	89	9	US-09-989-727-262	Sequence 262, App	
0.0	89	10	US-09-989-731-262	Sequence 262, App	
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0.0	89	10	US-09-991-073-262	Sequence 262, App	
0.0	89	10	US-09-990-442-262	Sequence 262, App	
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0.0	89	10	US-09-989-293A-262	Sequence 262, App	
0.0	89	10	US-09-989-735-262	Sequence 262, App	

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17	461	100.0	89	10	US-09-991-181-262	Sequence
18	461	100.0	89	10	US-09-989-730-262	Sequence
19	461	100.0	89	10	US-09-990-436-262	Sequence
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24	461	100.0	89	11	US-09-997-428-262	Sequence
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29	461	100.0	89	11	US-09-989-726-262	Sequence
30	461	100.0	89	11	US-09-998-156-262	Sequence
31	461	100.0	89	11	US-09-990-437-262	Sequence
32	461	100.0	89	11	US-09-991-157-262	Sequence
33	461	100.0	89	11	US-09-997-514-262	Sequence
34	461	100.0	89	11	US-09-997-573-262	Sequence
35	461	100.0	89	11	US-09-991-172-262	Sequence
36	461	100.0	89	11	US-09-990-726-262	Sequence
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ALIGNMENTS

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; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Kijavini, Ivar J.
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuc
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C63
; CURRENT APPLICATION NUMBER: US/09/989, 722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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ON NUMBER: 60/092182
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on, Dan L.
rara, Napoleone
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ritsen, Mary E.
dard, Audrey
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naldi, J. Christopher
ney, Austin L.
avin, Ivar J.
iet, Mary A.
James
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Margaret Ann
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as, Daniel
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i, William I.
ig, Zemin

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ION: Acids Encoding the Same
P2730PIC82

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ION NUMBER: 60/091478

; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
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RESULT 3

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; Sequence 262, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: KJavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nu
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C56
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; CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1997-10-17
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ang, Zemin
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Acids Encoding the Same
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ON NUMBER: 60/091626

PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 461; DB 9; Length 89;
Best Local Similarity 100.0%; Pred. No. 5.8e-48;
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RESULT 5
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eator, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuc
FILE REFERENCE: P2730FIC70
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CURRENT FILING DATE: 2001-11-20
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PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28

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100.0%; Score 461; DB 10; Length 89;
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enazi, Avi J.
er, Kevin P.
stein, David
noyers, Luc
on, Dan L.
rara, Napoleone
g, Sherman
ber, Hanspeter
ritsen, Mary E.
dard, Audrey
owski, Paul J.
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ney, Austin L.
avin, Ivar J.
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P2730P1C57

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TE: 1998-04-28

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ION NUMBER: 60/091982

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; PRIOR FILING DATE: 1998-07-09

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nu
; FILE REFERENCE: P2730PLC15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-06-02

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100.0%; Score 461; DB 10; Length 89;
Identity 100.0%; Pred. No. 5,8e-48;
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Kenazi, Avi J.
Ker, Kevin P.
Kestine, David
Knobers, Luc
Kon, Dan L.
Korara, Napoleone
Kong, Sherman
Korber, Hanspeter
Kritsen, Mary E.
Kiddard, Audrey
Kowalski, Paul J.
Krimaldi, J. Christopher
Kreney, Austin L.
Kjavin, Ivar J.
Kjier, Mary A.
Kjames,
Kjoni, Nicholas F.
Kjy, Margaret Ann
Kjewart, Timothy A.
Kjmas, Daniel
Kjtanabe, Colin K.
Kjlliams, P. Mickey
Kjod, William I.
Kjang, Zemin
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TION: Acids Encoding the Same
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; Sequence 262, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuc
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC17
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; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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enazi, Avi J.

er, Kevin P.

stein, David

noyers, Luc

on, Dan L.

rara, Napoleone

g, Sherman

ber, Hanspeter

ritsen, Mary E.

dard, Audrey

owski, Paul J.

mal, J. Christopher

ney, Austin L.

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ION: Secreted and Transmembrane Polypeptides and Nucleic

ION: Acids Encoding the Same

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100.0%; Score 461; DB 10; Length 89;
Larity 100.0%; Pred. No. 5.8e-48;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Goddard, Audrey
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nu
; FILE REFERENCE: P2730PIC22
; CURRENT APPLICATION NUMBER: US/09/990,456
; PRIOR FILING DATE: 2001-11-14
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ker, Kevin P.
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ng, Sherman
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ritsen, Mary E.
ddard, Audrey
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imaidi, J. Christopher
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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P2730PIC66

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/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: 60/089653
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/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
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/ PRIOR APPLICATION NUMBER: 60/089952
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/ PRIOR FILING DATE: 1998-06-22
/ PRIOR APPLICATION NUMBER: 60/090252
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/ PRIOR APPLICATION NUMBER: 60/090349
/ PRIOR FILING DATE: 1998-06-23
/ PRIOR APPLICATION NUMBER: 60/090355
/ PRIOR FILING DATE: 1998-06-23
/ PRIOR APPLICATION NUMBER: 60/090429
/ PRIOR FILING DATE: 1998-06-24

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ATE: 1998-06-24
ION NUMBER: 60/090435
ATE: 1998-06-24
ION NUMBER: 60/090444
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ION NUMBER: 60/090445
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ION NUMBER: 60/090472
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ION NUMBER: 60/091633
ATE: 1998-07-02
ION NUMBER: 60/091978
ATE: 1998-07-07
ION NUMBER: 60/091982
ATE: 1998-07-07
ION NUMBER: 60/092182
ATE: 1998-07-09

100.0%; Score 461; DB 10; Length 89;
Identity 100.0%; Pred. No. 5.8e-48;
Conservative 0; Mismatches 0; Indels 0; Caps 0;

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US2002019329A1
ION:
tenazi, Avi J.
cer, Kevin P.

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaten, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and N
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P27301C61
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-06-05

us-10-063-557-50.rapb

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;	PRIOR FILING DATE:	1998-07-02
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;	PRIOR APPLICATION NUMBER:	60/091982
;	PRIOR FILING DATE:	1998-07-07
;	PRIOR APPLICATION NUMBER:	60/092182
;	PRIOR FILING DATE:	1998-07-09

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DB	61	CKYSSQKHSPVPEKAIPLITPGSATTC 89

Search completed: January 6, 2004, 16:09:44
Job time : 32 secs

GenCore version 5.1.6
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in search, using sw model

uary 6, 2004, 16:01:30 ; Search time 21 Seconds
(without alignments)
407.572 Million cell updates/sec

-10-063-557-50

1 MERVTLALLLAGLTALEAN.....HSPVPEKALPLITPGSATTTC 89

OSUM62
pop 10.0 , Gapext 0.5

3308 seqs, 96168682 residues

is satisfying chosen parameters: 283308

3th: 0

3th: 2000000000

inimum Match 0%

aximum Match 100%

isting first 45 summaries

IR 76:*

Pir1:*

Pir2:*

Pir3:*

Pir4:*

the number of results predicted by chance to have a
c than or equal to the score of the result being printed,
ad by analysis of the total score distribution.

SUMMARIES

seq	Length	DB	ID	Description
5.6	87	2	I59391	transmembrane prot
2.4	88	2	S61552	mammary tumor prot
3.5	87	2	A55571	chloride conductan
7.4	92	2	A40533	CAMP-dependent pro
1.9	58	2	D46435	Na+/K+-exchanging
1.5	53	2	A46435	Na+/K+-exchanging
1.4	58	2	B46435	Na+/K+-exchanging
1.9	58	2	C46435	Na+/K+-exchanging
1.6	160	1	A61088	plastoquinol-plast
1.4	529	2	F69989	conserved hypothet
1.0	150	2	AH0371	probable membrane
1.6	135	2	A05009	hypothetical prote
1.4	359	2	A72004	chorismate synthas
1.4	359	2	B86620	chorismate synthas
1.4	523	2	A38101	potassium channel
1.3	446	2	B90463	potassium channel
1.9	525	2	A43531	potassium channel
1.8	309	2	AC1697	probable transport
1.8	309	2	AI1325	probable transport
1.8	511	2	A46020	potassium channel
1.8	511	2	S07095	potassium channel
1.8	585	2	A39395	delayed rectifier
1.8	620	2	A70525	hypothetical prote
1.7	468	2	C96818	hypothetical prote
1.6	239	2	A38111	transcription regu
1.6	679	2	A42073	potassium channel
1.6	769	2	I56546	Shaw type potassiu
1.6	910	2	F81974	leucine-tRNA ligas
1.4	381	2	AB2907	GGDEF family prote

30 62 13.4 393 2 B97682 ggdef fami
31 62 13.4 589 2 T43295 uracil tra
32 62 13.4 777 2 S30271 pyocin AP4
33 61.5 13.3 342 2 S75086 iron-stres
34 61.5 13.3 433 2 H86597 flagellum-
35 61.5 13.3 433 2 B72025 flagellum-
36 61.5 13.3 433 2 A81513 virulence
37 61.5 13.3 445 2 AD0962 DsdX perme
38 61.5 13.3 1499 2 AC2555 hypothetic
39 61 13.2 268 2 C87295 conserved
40 61 13.2 355 2 T51137 major hist
41 61 13.2 461 2 B90984 O antigen
42 61 13.2 463 2 A75151 damage-ind
43 61 13.2 463 2 G71191 probable D
44 61 13.2 463 2 E85829 O antigen
45 61 13.2 520 2 D84471 O antigen
prbable me

ALIGNMENTS

RESULT 1
I59391
transmembrane protein - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov
C/Accession: I59391
R/Attali, B.; Latter, H.; Rachamim, N.; Garty, H.
Proc. Natl. Acad. Sci. U.S.A. 92, 6092-6096, 1995
A/Title: A corticosteroid-induced gene expressing an 'IsK-like' K+ cha
A/Reference number: I59391; MUID:95320221; PMID:7597086
A/Accession: I59391
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-87 <RES>
A/Cross-references: GB:L41254; NID:G951422; PIDN:AAA74691.1; PID:G9514
C/Genetics:
A/Gene: 3D CHIF

Query Match 55.6%; Score 256.5; DB 2; Length 87;
Best Local Similarity 61.5%; Pred. No. 2.8e-21;
Matches 56; Conservative 11; Mismatches 17; Indels 7; G

Qy 1 MERVTLA-LLLLAGLTALEANDFANKDPFYVDWKNLQSLGICGLIAIGTAA
Db 1 MEGITCAFLIVLAGLPVLEANGP-VKGSFPFYDWSLQLGMIFGGLLCIAGIAM
Qy 60 KCKYKSSQKHSP--VPEKALPLITPGSATT 88
Db 60 KCK---CRRNHTPSSLPEKVTPLITPGSAST 87

RESULT 2
S61552
mammary tumor protein mat8 precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 05-Nov
C/Accession: S61552; I48648
R/Morrison, B.W.; Leder, P.
Oncogene 9, 3417-3426, 1994
A/Title: neu and ras initiate murine mammary tumors that share genetic
A/Reference number: I48271; MUID:95060797; PMID:7970700
A/Accession: S61552
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-88 <MOR>
A/Cross-references: EMBL:X93038; NID:G1085067; PIDN:CAA63606.1; PID:GI
C/Genetics:
A/Gene: mat8
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-88/Product: mammary tumor protein mat8 #status predicted <MAT>
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Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 19-AJ
A:Accession: D46435; S31525
R:Mercer, R.W.; Biemesderfer, D.; Bliss Jr., D.P.; Collins, J.H.; Fox,
J. Cell Biol 121, 579-586, 1993
A>Title: Molecular cloning and immunological characterization of the
A:Reference number: A46435; MUID:93252993; PMID:8387529
A:Accession: D46435
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-58 <MER>
A:Cross-references: EMBL:X70059; NID:g936; PIDN:CAA49663.1; PID:g9397
A>Note: The authors translated the codon TTC for residue 25 as Pro
C:Keywords: hydrolase; transmembrane protein

Query Match 20.9%; Score 96.5; DB 2; Length 58;
Best Local Similarity 34.6%; Pred. No. 0.00093;
Matches 18; Conservative 14; Mismatches 19; Indels 1;

QY 27 DDPPFYDKNLQSLGICGLLIAAGTAAVLGSKCKYSQKHSPVPEKAI 78
:|||||::: |||| |::: |||| |::: |||| |::: |||| |:::
Db 8 EDPPFYDYETVRNGGLIPAALAFIVGLVIILSKRFRC-GAKKKHQIPEDGL 51

RESULT 6
A46435
Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - sheep (fragment)
N:Alternate names: sodium pump gamma chain; sodium/potassium-depender
C:Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)
C>Date: 22-Nov-1993 #sequence_revision 05-Dec-1998 #text_change 19-AJ
A:Accession: A46435; S31524; A27383
R:Mercer, R.W.; Biemesderfer, D.; Bliss Jr., D.P.; Collins, J.H.; Fox,
J. Cell Biol 121, 579-586, 1993
A>Title: Molecular cloning and immunological characterization of the
A:Reference number: A46435; MUID:93252993; PMID:8387529
A:Accession: A46435
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 6-53 <MER>
A:Experimental source: kidney
A>Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:131232, NCBIP:131232)
R:Mercer, R.W.
submitted to the EMBL Data Library, December 1992
A:Description: Cloning and sequencing of gamma subunit of sodium potas
A:Reference number: S31522
A:Accession: S31524
A:Molecule type: mRNA
A:Residues: 6-19,'F',21-53 <MEW>
A:Cross-references: EMBL:X70061; NID:g1255; PIDN:CAA49665.1; PID:g1255
R:Collins, J.H.; Leszyk, J.
Biochemistry 26, 8665-8668, 1987
A>Title: The "gamma-subunit" of Na,K-ATPase: a small, amphiphilic pro
A:Reference number: A27383; MUID:88163544; PMID:2831947
A:Accession: A27383
A:Molecule type: Protein
A:Residues: 1-19,'F',21-33 <COL>
C:Complex: heterotrimer; alpha, beta, and gamma chain
C:Keywords: heterotrimer; hydrolase; transmembrane protein

Query Match 20.5%; Score 94.5; DB 2; Length 53;
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Matches 18; Conservative 14; Mismatches 19; Indels 1;

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Ddb 3 EDPPFYDYETVRNGGLIPAALAFIVGLVIILSKRFRC-GAKKKHQIPEDGL 53

RESULT 7
S34635
Na+/K+-exchanging ATPase (EC 3.6.3.9) gamma chain - rat

norvegicus (Norway rat)
 #sequence_revision 03-Feb-1994 #text_change 19-Apr-2002
 5; S31523
 emesederfer, D.; Bliss Jr., D.P.; Collins, J.H.; Forbush III, B.
 579-586, 1993
 cloning and immunological characterization of the gamma polypeptide,
 A46435; MUID:93252993; PMID:8387529
 5
 ary
 RNA
 MER>
 : EMBL:X70062; NID:g56299; PIDN:CAA49666.1; PID:g56300
 s translated the codon TTC for residue 25 as Pro
 ase; transmembrane protein
 16.4%; Score 75.5; DB 2; Length 58;
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 conservative 12; Mismatches 19; Indels 1; Gaps 1;
 YYDWKNLQSLGCGLLAAGIAAVLSGCKYKSKQKHSVPVE 75
 EYDVTVRKGLIFAGLAFVVGLLILSKRFRCCGS-KKRRQVNE 55
 5
 ATPase (EC 3.6.3.9) gamma chain - mouse
 culus (house mouse)
 3 #sequence_revision 03-Feb-1994 #text_change 19-Apr-2002
 5; S31522
 emesederfer, D.; Bliss Jr., D.P.; Collins, J.H.; Forbush III, B.
 579-586, 1993
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 5
 ary
 RNA
 MER>
 : EMBL:X70060; NID:g51111; PIDN:CAA49664.1; PID:g51112
 s translated the codon TTC for residue 25 as Pro
 ase; transmembrane protein
 15.9%; Score 73.5; DB 2; Length 58;
 arity 32.7%; Pred. No. 0.33; Mismatches 20; Indels 1; Gaps 1;
 conservative 12; Mismatches 20; Indels 1; Gaps 1;
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 EYDVTVRKGLIFAGLAFVVGLLILSKRFRCCGS-KKRRQVNE 55
 5
 ocyanin reductase (EC 1.10.99.1) 17K protein - Synechocystis sp. (stra
 cytochrome b6-f complex chain IV; plastoquinol-plastocyanin reductase
 cystis sp.
 3
 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
 8; S76298; S15474
 57, 336-342, 1992
 ion of insertion mutants of Synechocystis sp. PCC 6803: evidence for a
 : A61088; MUID:92272582; PMID:11590707
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 NA
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 : EMBL:X58522; NID:947376; PIDN:CAA41412.1; PID:g47377
 : S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 : Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 6, 1996
 analysis of the genome of the unicellular cyanobacterium Synechocystis
 : S74322; MUID:97061201; PMID:8905231

A:Accession: S76298
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-160 <KAN>
 A:Cross-references: EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAAL
 A:Note: the nucleotide sequence was submitted to the EMBL Data Librar
 C:Genetics:
 A:Gene: petD
 C:Superfamily: plastoquinol-plastocyanin reductase 17K protein; plast
 C:Keywords: oxidoreductase; photosynthesis; thylakoid
 F:24-144/Domain: plastoquinol-plastocyanin reductase 17K protein homo
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 Best Local Similarity 37.7%; Pred. No. 1.4;
 Matches 23; Conservative 9; Mismatches 21; Indels 8;
 QY 7 ALLLAGLTAI-----EANDPFANKD--PFYYDWKNLQSLGCGLLAAGI
 Db 47 ALGIAGLAILDPAIMIGEPADFFATPEILPEWVLYPTFQILRLPNKLLGIAGW
 QY 59 G 59
 Db 107 G 107
 RESULT 10
 F69989
 conserved hypothetical protein ytcJ - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun
 C:Accession: F69989
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; J
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.;
 A.; Ehrlich, S.D.; Emmerison, P.T.; Entian, K.D.; Errington, J.; Fabret
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; C
 tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosor
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapi
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.;
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.;
 A:Authors: Schleich, S.; Schroter, R.; Scoffone, F.; Sekiguchi, J.; S
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terstra, P.; Tognoni, A.; Tos
 I.; Winers, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Ye
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium E
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: F69989
 A:Status: preliminary; nucleic acid sequence not shown; translation nc
 A:Molecule type: DNA
 A:Residues: 1-529 <KUN>
 A:Cross-references: GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB1493
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: ytcJ
 Query Match 15.4%; Score 71; DB 2; Length 529;
 Best Local Similarity 30.4%; Pred. No. 6.2;
 Matches 31; Conservative 9; Mismatches 24; Indels 38; G
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 Db 381 ALDLPQHFVASFDFWVDRIGKDRMKTAFAWKTLISKGLCAAGSDAPIEPVDPLL
 QY 53 IAAVLSGCKVKSKQKHS-----VP-EKAIPITPGSA 86
 Db 440 -SAVLR-----KSSHEQNGFSYNESECLPVYEAIKLYTEGSA 475
 RESULT 11
 AH0371
 Probable membrane protein YPO3057 [imported] - Yersinia pestis (strain
 C:Species: Yersinia pestis

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001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
71
ren, B.W.; Thomson, N.R.; Titball, R.W.; Hoiden, M.T.G.; Prentice, M.B.
l.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
d, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
;27, 2001
sequence of Yersinia pestis, the causative agent of plague.
=: AB0001; MUID:21470413; PMID:11586360
71
nary
DNA
) <KUR>
=: GB:AL590842; PIDN:CAC92299.1; PID:g15981010; GSFDB:GN00175
'pothetical protein ytw1
    15.0%; Score 69; DB 2; Length 150;
larity 30.2%; Pred.No.2.8;
Conservative 14; Mismatches 32; Indels 14; Gaps 4;
ALLLAGLTALEANDPFANKDDPFYDWNQLQSLGICGGLLAIAGI-AAVLGSCKC 62
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
AIIILIAIRITPLNS-----FFPK--VEKYGLTIGVLIITGVWAPIASG--K 72
SQQHSPVPPEKAIPLTGPSATT 88
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
SEVLHSFQWKSIILAIVGVAVS 98
ein 135 - liverwort (Marchantia polymorpha) chloroplast
plast Marchantia polymorpha
87 #sequence_revision 05-Jun-1987 #text_change 08-Oct-1999
71: A05009
okuchi, H.; Shiki, Y.; Takeuchi, M.; Chang, Z.; Fukuzawa, H.; Kohchi,
, 299-331, 1988
e and organization of Marchantia polymorpha chloroplast genome. II. Gen
r: S01567; MUID:89068696; PMID:2974085
71
DNA
<UNE>
s: EMBL:X04465; NID:g11640; PIDN:CAA28060.1; PID:g453590
uzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shi
74, 1996
ast gene organization deduced from complete sequence of liverwort March
r: A38014
ation; gene organization, sites, features
last
pothetical protein 135
oplast
    14.6%; Score 67.5; DB 2; Length 135;
larity 32.6%; Pred.No.3.7;
Conservative 11; Mismatches 13; Indels 7; Gaps 2;
AG--LTALEANDPFANKDDPFYDWNQLQSLGICGGLLAIAG 52
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
IGLFYALKRPEPVSRDYDFFF-----SCIGLLCGGILLFFQG 56
se CP0815 [imported] - Chlamydomophila pneumoniae (strains CWL029 and AR3
dophila pneumoniae, Chlamydia pneumoniae
99 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
04: D81536
chell,W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
385-389, 1999
ive genomes of Chlamydia pneumoniae and C. trachomatis.
```

January 6, 2004, 16:04:40

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

.n search, using sw model

wary 6, 2004, 16:00:10 ; Search time 11 Seconds
(without alignments)
380.489 Million cell updates/sec

10-063-557-50

ERTVTLALLLAGLTALEANDPFAKDDPFYVDWKNLQSLGICGGLLAIAAGAAV

863 seqs, 47026705 residues
s satisfying chosen parameters: 127863

lth: 0
rth: 2000000000

minimum Match 0%

Maximum Match 100%

string first 45 summaries

MissProt_41:*

the number of results predicted by chance to have a

than or equal to the score of the result being printed,

ed by analysis of the total score distribution.

SUMMARIES

Ch	Length	DB	ID	Description
1	89	1	FXV4 HUMAN	P59646 homo sapien
2	88	1	FXV4 MOUSE	Q9d2w0 mus musculus
3	87	1	FXV4 RAT	Q63113 rattus norv
4	88	1	FXV3 MOUSE	Q61835 mus musculus
5	88	1	FXV3 RAT	P59645 rattus norv
6	88	1	FXV3 PIG	Q97797 sus scrofa
7	87	1	FXV3 HUMAN	Q14802 homo sapien
8	92	1	PLM HUMAN	Q00168 homo sapien
9	92	1	PLM CANFA	P56513 canis famil
10	94	1	FXV6 RAT	Q91xv6 rattus norv
11	94	1	FXV6 MOUSE	Q9d164 mus musculus
12	92	1	PLM MOUSE	Q92239 mus musculus
13	92	1	PLM RAT	Q08589 rattus norv
14	95	1	FXV6 HUMAN	Q9h0g3 homo sapien
15	58	1	ATNG BOVIN	Q04645 bos taurus
16	53	1	ATNG SHEEP	Q04680 ovis aries
17	178	1	FXV5 HUMAN	Q96db9 homo sapien
18	178	1	FXV5 RAT	P59647 rattus norv
19	80	1	FXV7 HUMAN	P58549 homo sapien
20	80	1	FXV7 MOUSE	P59648 mus musculus
21	66	1	ATNG HUMAN	P54710 homo sapien
22	80	1	FXV7 RAT	P59649 rattus norv
23	86	1	ATNG RAT	Q04679 rattus norv
24	70	1	ATNG MOUSE	Q04646 mus musculus
25	93	1	FXV8 HUMAN	P58550 homo sapien
26	160	1	PETD SVNY3	P27589 synchocyst
27	61	1	ATNG XENLA	Q13001 xenopus lae
28	184	1	FXV5 MOUSE	P97808 mus musculus
29	135	1	YC66 MARPO	Q32616 marchantia
30	330	1	AROC SULFO	Q96v94 sulfolobus
31	359	1	AROC CHLPN	Q926m2 chlamydia p
32	523	1	CIK3 HUMAN	P22001 homo sapien
33	525	1	CIK3 RAT	P15384 rattus norv

34	63.5	13.8	511	1	KNC1 HUMAN	P48547 homo
35	63.5	13.8	511	1	KNC1 MOUSE	P15388 mus
36	63.5	13.8	585	1	KNC1 RAT	P25122 ratt
37	62.5	13.6	299	1	COMQ BACSU	P33690 baci
38	62.5	13.6	769	1	KNC3 MOUSE	O63959 mus
39	62.5	13.6	910	1	SYL NEIMA	Q9jw39 neis
40	62.5	13.6	1048	1	SILA SALTY	Q9zhc9 salm
41	62	13.4	581	1	PUR4 SCHPO	Q10279 schi
42	61.5	13.3	342	1	ISIA SVNY3	O52274 syne
43	61.5	13.3	524	1	P60 LISIV	Q01837 list
44	60.5	13.1	638	1	KNC2 RAT	P22462 ratt
45	60.5	13.1	728	1	PURL CANJE	Q9pny0 camp

ALIGNMENTS

RESULT 1
FXV4 HUMAN STANDARD; PRT; 89 AA.
AC P59646;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE FXVD domain-containing ion transport regulator 4 precursor.
GN FXVD4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP RECONSTRUCTION FROM ESTS, AND CONCEPTUAL TRANSLATION.
RX MEDLINE-20408885; PubMed-10950925;
RA Sweadner K.J.; Rael E.;
RT "The FXVD gene family of small ion transport regulators or channe
RT cDNA sequence, protein signature sequence, and expression.";
RL Genomics 68:41-56(2000).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -|- SIMILARITY: Belongs to the FXVD family.
CC This SWISS-PROT entry is copyright. It is produced through a coll;
CC between the Swiss Institute of Bioinformatics and the EMBL Out;
CC the European Bioinformatics Institute. There are no restriction;
CC use by non-profit institutions as long as its content is in
CC modified and this statement is not removed. Usage by and for c
CC entities requires a license agreement (See <http://www.isb-sib.ch/>;
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: A1829357 -; NOT ANNOTATED_CDS.
DR Genew; HGNC:4028; FXVD4.
DR PROSITE: PS01310; FXVD; 1.
KW Transmembrane; Signal; Ionic channel; Ion transport.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 89 FXVD DOMAIN-CONTAINING ION TRANSPORT
FT DOMAIN 21 38 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 39 59 POTENTIAL.
FT DOMAIN 60 89 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 89 AA; 9373 MW; B595EF99A4949B4 CRC64;
Query Match 97.6%; Score 450; DB 1; Length 89;
Best Local Similarity 97.8%; Pred. No. 8.8e-41;
Matches 87; Conservative 1; Mismatches 1; Indels 0; G;
QY 1 MERVTLALLLAGLTALEANDPFAKDDPFYVDWKNLQSLGICGGLLAIAAGAAV
Db 1 MERVTLALLLAGLTALEANDPFAKDDPFYVDWKNLQSLGICGGLLAIAAGAAV
QY 61 CKYKSSQKHSPVPEKAIPITPGSATTC 89

||||| KSKQKSHSPVPEKAIPITPGSATTC 89

STANDARD; PRT; 89 AA.

(Rel. 41, Created)

(Rel. 41, Last sequence update)

(Rel. 41, Last annotation update)

containing ion transport regulator 4 precursor (Channel

tor) (CHIF).

(Mouse).

Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

0090;

M N.A.

VJ;

ence of mouse CHIF (FXVD4).";

AR-2001) to the EMBL/GenBank/DBJ databases.

M N.A.

/6J; TISSUE=Kidney;

5660; PubMed=11217851;

Inagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

zawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

azaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

atsuda H.A., Ashburner M., Batalov S., Casavant T.,

W., Gaasterland T., Gissi C., King B., Kochiwa H.,

wis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,

ido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

ifelli D., Bojunga N., Carinci P., de Bona M.F.,

J.F., Bult C., Fletcher C., Fujita M., Gariboldi M.,

rchioni L., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

ato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

oyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

S.A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Y.;

annotation of a full-length mouse cDNA collection.";

85-690(2001).

LAR LOCATION: Type I membrane protein (Potential).

TY: Belongs to the FXVD family.

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Swiss Institute of Bioinformatics and the EMBL outstation -

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mail to license@isb-sib.ch).

29; AAK51508.1; -

28; BAB31372.1; -

9005; FXVD4

R00272; ATP1G1_PLM_MAT8.

8; ATP1G1_PLM_MAT8; 1.

1310; FXVD; 1.

e; Signal; Ionic channel; Ion transport.

21 20 POTENTIAL.

FXVD DOMAIN-CONTAINING ION TRANSPORT

REGULATOR 4.

21 38 EXTRACELLULAR (POTENTIAL).

39 59 POTENTIAL.

60 88 CYTOPLASMIC (POTENTIAL).

8 AA; 9269 MW; 7EB0140941CFE926 CRC64;

Query Match 60.0%; Score 276.5; DB 1; Length 88;
Best Local Similarity 66.7%; Pred. No. 1.7e-22;
Matches 60; Conservative 8; Mismatches 19; Indels 3;

QY 1 MERVTLA-LLLLAGLTALEANDPFANKDDPFYDYWKNLQSLGGLGIIAGI?
Db 1 MEEITCAFLLLAGLPALEASDP-VDKSPFYDYWESLQGLGIIAGI?
QY 60 KCKYKSKQKSHSPVPEKAIPITPGSATTC 89
Db 60 KCKRRTHKP-SSLPKATPLIIPGSANTC 88

RESULT 3

FXV4 RAT

ID_FXV4 RAT

AC Q63113; STANDARD; PRT; 87 AA.

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE FXVD domain-containing ion transport regulator 4 precursor (Char

DE inducing factor) (CHIF) (Corticosteroid-induced protein).

GN FXVD4.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ra

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Mistar; TISSUE=Colon;

RX MEDLINE=95320221; PubMed=7597086;

RA Attali B., Latter H., Rachamim N., Garty H.;

RT "A corticosteroid-induced Gene expressing an 'Isk-like' K+ chanr

activity in Xenopus oocytes";

RL Proc. Natl. Acad. Sci. U.S.A. 92:6092-6096(1995).

RN [2]

RP TISSUE SPECIFICITY.

RX MEDLINE=97000648; PubMed=8843704;

RA Capurro C., Coutry N., Bonvalet J.-P., Escoubert B., Garty H.,

Farman N.;

RT "Cellular localization and regulation of CHIF in kidney and colic

Am. J. Physiol. 271:C753-C762(1996).

CC -1- FUNCTION: Induces a potassium channel when expressed in xenc

oocytes.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

CC -1- TISSUE SPECIFICITY: Selectively present in the distal parts

nephron (medullary and papillary collecting ducts and end pc

of cortical collecting tubule) and in the epithelial cells c

distal colon. No expression is found in renal proximal tubul

loop of henle and distal tubule, proximal colon, small intes

lung, choroid plexus, salivary glands, or brain.

CC -1- INDUCTION: By corticosteroids.

CC -1- SIMILARITY: Belongs to the FXVD family.

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use by non-profit institutions as long as its content is i

modified and this statement is not removed. Usage by and for

entities requires a license agreement (See <http://www.isb-sib.ch>

or send an email to license@isb-sib.ch).

CC -----

CC EMBL: L41254; AAA74691.1; -

DR PIR: I59391; I59391.

DR InterPro: IPR030272; ATP1G1_PLM_MAT8.

DR Pfam: PF02638; ATP1G1_PLM_MAT8; 1.

DR PROSITE: PS01310; FXVD; 1.

Transmembrane; Signal; Ionic channel; Ion transport.

FT SIGNAL 1 20 POTENTIAL.

FT CHAIN 21 87 FXVD DOMAIN-CONTAINING ION TRANSPOR

REGULATOR 4.

FT DOMAIN 21 38 EXTRACELLULAR (POTENTIAL).

```

39 59 POTENTIAL.
60 87 CYTOPLASMIC (POTENTIAL).
AA: 9084 MW: 5D0DE1FFC61BCA CRC64;
arity 55.6%; Score 256.5; DB 1; Length 87;
conservative 11; Mismatches 17; Indels 7; Gaps 4;

TLA-LLLAGLTALEANDPPANKDPPFYDWNKQLSLGCGGLATAGIAVLGS 59
||||| ||||| : ||||| : ||||| : ||||| : ||||| : |||||
ICAFLLVLGLPVLNANP-VDKGSPFYDWSLQGLGMIFGGLICAGIAVALSG 59
KSSQKQHP--VPEKAIPLTGSAAT 88
:: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
--CRNHTPSLPEKVTPLTPGSAST 87

STANDARD; PRT; 88 AA.

Rel. 36, Created)
Rel. 36, Last sequence update)
Rel. 42, Last annotation update)
containing ion transport regulator 3 precursor (Chloride
inducer protein Mat-8) (Mammary tumor 8 kDa protein)
1-like).
OR FLML.
(Mouse).
azooa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
390;

N.A.
TISSUE=Breast;
797; PubMed=7970700;
Leder P.;
initiate murine mammary tumors that share genetic
ally absent in c-myc and int-2-initiated tumors.";
17-3426(1994).

N.A.
tumor;
257; PubMed=12477932;
G., Feingold E.A., Grouse L.H., Derge J.G.,
Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Tuellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Ewan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Con E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
idan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Touchman J.W., Green E.D., Dickson M.C.,
Grimwood J., Schmutz J., Myers R.M.,
S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
Schein J.E., Jones S.J.M., Marra M.A.,
ad initial analysis of more than 15,000 full-length
se cDNA sequences.";
Cad. Sci. U.S.A. 99:16099-16903(2002).

184; PubMed=7836447;
Moorman J.R., Kowdley G.C., Kobayashi Y.M., Jones L.R.,
al phospholeman-like protein expressed in human breast
es a chloride conductance in Xenopus oocytes.";
. 270:2176-2182(1995).
Induces a hyperpolarization-activated chloride current

```

when expressed in xenopus oocytes. May be a modulator capable activating endogenous oocyte channels.

-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

-!- TISSUE SPECIFICITY: Expressed in a subset of murine breast ti

-!- MISCELLANEOUS: Marker of a cell type preferentially transform neu or ras oncogene.

-!- SIMILARITY: Belongs to the FXD family.

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EMBL; X93038; CAA63606.1; --

EMBL; BC020339; AA020339.1; --

PIR; S61552; S61552.

MGD; MGI:107497; Fxyd3.

InterPro; IPR00272; ATP1G1_PLM_MAT8.

Pfam; PF02038; ATP1G1_PLM_MAT8; 1.

PROSITE; PS01313; FXYD; 1.

Transmembrane; Signal; Ionic channel; Chloride channel; Chloride; Ion transport.

FT SIGNAL 1 20 POTENTIAL.

FT CHAIN 21 88 FXYD DOMAIN-CONTAINING ION TRANSPORT REGULATOR 3.

FT DOMAIN 21 38 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 39 59 POTENTIAL.

FT DOMAIN 60 88 CYTOPLASMIC (POTENTIAL).

SQ SEQUENCE 88 AA; 9526 MW; 9CD61684B856E35D CRC64;

Query Match 52.4%; Score 241.5; DB 1; Length 88;

Best Local Similarity 57.8%; Pred. No. 8.5e-19;

Matches 52; Conservative 11; Mismatches 24; Indels 3; G

Qy 1 MERVTLALL-LLAGLTALEANDPPANKDPPFYDWNKQLSLGCGGLATAGIAA

Db 1 MQEVLVLLVLAGLPTLDANDP-ENKNDPPFYDWSYLRVGLICAGILCALGIIV

Qy 60 KCKYKSSQKHSPVPEKAIPLTPGSATTC 89

Db 60 KCKKFRQKP-SHRPGEGPLITPGSAHNC 88

RESULT 5

FXY3 RAT

ID "FXY3_RAT STANDARD; PRT; 88 AA.

AC PS9645;

DT 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE FXYD domain-containing ion transport regulator 3 precursor.

GN FXYD3.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RA Lee N.H., Glodek A., Chandra I., Mason T.M., Quackenbush J.,

RA Kerlavage A.R., Adams M.D.;

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP RECONSTRUCTION FROM ESTS, AND CONCEPTUAL TRANSLATION.

RX MEDLINE=20408885; PubMed=10950925;

RA Sweadner K.J., Rael E.;

RT "The FXYD gene family of small ion transport regulators or channe

RL cDNA sequence, protein signature sequence, and expression.";

RL Genomics 68:41-56(2000).

CC -!- FUNCTION: Induces a hyperpolarization-activated chloride curr

CC -!- WHEN EXPRESSED IN XENOPUS OOCYTES. MAY BE A MODULATOR CAPABLE

ng endogenous oocyte channels.
 LAR LOCATION: Type I membrane protein (Potential).
 FY: Belongs to the FYXD family.

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65: -; NOT ANNOTATED CDS.
 R000272; ATP1G1_PLM_MAT8.
 8; ATP1G1_PLM_MAT8; 1.
 1310; FYXD; 1.
 e; Signal; Ionic channel; Ion transport.

1 20
 21 88
 21 38
 39 59
 60 88
 8 AA; 9411 MW; 45APE872FDIAF944 CRC64;

larity 50.9%; Score 234.5; DB 1; Length 88;
 Conservativity 10; Mismatches 26; Indels 3; Gaps 3;

VTLLALL-LLAGLTALANDPFPYDWNKQLSLGGLGGLAIAAGI 59
 FALSLLVLLAGLTLDNDP-EDKDSFPYDWHSLRVGLGGLICAGLGIIVLMSG 59
 YKSQKHSPVPEKAIPITPGSATTC 89
 CKFSQKP-SHRPGDGPLITPGSAHNC 88

STANDARD; PRT; 88 AA.
 (Rel. 41, Created)
 (Rel. 41, Last sequence update)
 (Rel. 41, Last annotation update)
 containing ion transport regulator 3 precursor (Chloride inducer protein Mat-8) (Mammary tumor 8 kDa protein).
 8.
 Pig).
 etazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cheria; Cetartiodactyla; Suina; Suidae; Sus.
 823;
 M N.A.
 ic mucosa;
 0476; PubMed=10206733;
 nano X., Hirano Y., Suzuki M., Takahashi E.-I., Terada T., Co R.;
 of P-type transporting ATPases and chromosomal locations es.";
 Funct. 23:315-323(1998).
 : Induces a hyperpolarization-activated chloride current ressed in xenopus oocytes. May be a modulator capable of ng endogenous oocyte channels.
 LAR LOCATION: Type I membrane protein (Potential).
 FY: Belongs to the FYXD family.

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or send an email to license@isb-sib.ch.

CC EMBL; AB015759; BAA35078.1; -;
 CC InterPro; IPR000272; ATP1G1_PLM_MAT8.
 DR Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
 DR PROSITE; PS01310; FYXD; 1.
 KW Transmembrane; Signal; Ionic channel; Chloride channel; Chloride ion transport.
 FT SIGNAL 1 17 POTENTIAL
 FT CHAIN 18 88
 FT FYXD DOMAIN-CONTAINING ION TRANSPORT
 FT REGULATOR 3.
 FT DOMAIN 18 38 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 39 59 POTENTIAL.
 FT DOMAIN 60 88 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 88 AA; 9314 MW; 6CC7810B90512E5A CRC64;

Query Match 50.0%; Score 230.5; DB 1; Length 88;
 Best Local Similarity 57.8%; Pred. No. 1.2e-17;
 Matches 52; Conservativity 10; Mismatches 25; Indels 3;

QY 1 MERVTLA-LILLAGLTALANDPFPYDWNKQLSLGGLGGLAIAAGI 59
 Db 1 MHEVALSVLLAGLSALDNDP-EDKNSFPYDWHSLRVGLGGLICAGTGPCALGII 59
 QY 60 KCKYKSQKHSPVPEKAIPITPGSATTC 89
 Db 60 KCKKFSQKP-SHRPGDAPPLITPGSAHDC 88

RESULT 7
 ID FXY3_HUMAN STANDARD; PRT; 87 AA.
 AC Q14802; Q13211;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE FYXD domain-containing ion transport regulator 3 precursor (Chlc conductance inducer protein Mat-8) (Mammary tumor 8 kDa protein)
 DE (Phospholemman-like).
 GN FYXD3 OR MAT8 OR PLML.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95138134; PubMed=7836447;
 RA Morrison B.W., Moorman J.R., Kowdley G.C., Kobayashi Y.M., Jones Leder P.;
 RA "Mat-8, a novel phospholemman-like protein expressed in human br tumors, induces a chloride conductance in Xenopus oocytes.";
 RL J. Biol. Chem. 270:2176-2182(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung carcinoma;
 RA Lei W., Wu M.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Urinary bladder;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G. Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz R. Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk Villalón D.K., Morley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

GN FX1D1 OR PLM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=97312702; PubMed=9169143;
 RA Chen L.-S.K., Lo C.F., Numann R., Cuddy M.;
 RT "Characterization of the human and rat phospholemman (PLM) cDNAs
 RT localization of the human PLM gene to chromosome 19q13.1";
 RL Genomics 41:435-443 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20408885; PubMed=10950925;
 RA Sweadner K.J., Rael E.;
 RT "The FX1D gene family of small ion transport regulators or channel
 RT cDNA sequence, protein signature sequence, and expression.";
 RL Genomics 68:41-56 (2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Lung, and Testis;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.I.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.F.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.,
 RA Villalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Hulyk S.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.U.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- FUNCTION: Induces a hyperpolarization-activated chloride current
 CC when expressed in xenopus oocytes. May have a functional role
 CC in muscle contraction.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Highest expression in skeletal muscle and
 CC heart. Moderate levels in brain, placenta, lung, liver, pancreas,
 CC uterus, bladder, prostate, small intestine and colon with mucosal
 CC lining. Very low levels in kidney, colon and small intestine
 CC without mucosa, prostate without endothelial lining, spleen,
 CC testis.
 CC -!- PTM: Major plasma membrane substrate for camp-dependent protein
 CC kinase (PK-A) and protein kinase C (PK-C) in several different
 CC tissues (By similarity). Phosphorylated in response to insulin
 CC adrenergic stimulation.
 CC -!- SIMILARITY: Belongs to the FX1D family.
 CC -----
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 CC -----
 CC EMBL: U72245; AAC51286.1; -;
 CC EMBL: BC032800; AAH32800.1; -;
 CC Genbank: HGNC:4025; FX1D1.
 CC MIM: 602359; -;
 CC DR GO: 00005887; C:integral to plasma membrane; TAS.
 CC DR

54; F:chloride channel activity; TAS.
121; P:chloride transport; TAS.
336; P:muscle contraction; TAS.
R000272; ATP1G1.PLM.MAT8.
18; ATP1G1.PLM.MAT8; 1.
1310; FXVD; 1.
e; Phosphorylation; Signal; Ionic channel;
annel; Chloride; Ion transport.
1 20
BY SIMILARITY.
21 92
PHOSPHOLEMMAN.
21 35
EXTRACELLULAR (POTENTIAL).
36 56
POTENTIAL.
57 92
CYTOPLASMIC (POTENTIAL).
83 88
PHOSPHORYLATION (BY PKC AND PKA).
88 83
PHOSPHORYLATION (BY PKA).
3 3
S -> P (IN REF. 1).
5 5
G -> H (IN REF. 1).
2 AA; 10441 MW; 11602EFAFFDBD8 CRC64;
28.0%; Score 129; DB 1; Length 92;
larity 41.3%; Pred. No. 6.5e-07;
Conservative 15; Mismatches 20; Indels 2; Gaps 1;
LEANDRPANKDDPPYDKMLQLSLGICGLLATAGIAANVLGCKYKSSQKHSPV 73
AKAESP--KEHDPPTYDQSLQIGLVIAFILFGLHILVLSRRCRCKFNQOQTGE 72
76
75
STANDARD; PRT; 92 AA.
(Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 41; Last annotation update)
n precursor (FXVD domain-containing ion transport
aris (Dog).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Carnivora; Fissipedia; Canidae; Canis.
615;
M N.A., AND SEQUENCE OF 21-92.
icular muscle; 1710217;
0422; PubMed:1710217;
Scott B.T., Jones L.R.;
n and complete sequence determination of the major plasma
strate for CAMP-dependent protein kinase and protein
myocardium";
m. 266:11126-11130(1991).
ressed in xenopus oocytes. May have a functional role in
ontraction.
LAR LOCATION: Type I membrane protein.
PECIFICITY: Present in heart, esophagus, stomach, aorta,
muscle, smooth muscle, and liver but absent from brain
ey.
or plasma membrane substrate for camp-dependent protein
PK-A) and protein kinase C (PK-C) in several different
Phosphorylated in response to insulin and adrenergic
ion (By similarity)
TY: Belongs to the FXVD family.
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8; BAB62242.1; --
9; AAF66613.1; --
300272; ATP1G1_PLM_MAT8.
310; FXVD; 1;
Signal; Ionic channel; Ion transport;
plicing.
1 17
18 34
35 57
58 94
20 20
65 65
AA; 10398 MW; 1C0D35FA0C572451 CRC64;
27.0%; Score 124.5; DB 1; Length 94;
arity 37.5%; Pred. No. 2e-06;
onservative 15; Mismatches 37; Indels 3; Gaps 2;
TLALLLAGTALFANDPFANKDPFYDKNQLSLGGLGGLAIAAGIAVLSGK 60
LILCSLLAPVVLASAEKEK-DFFYYDQTLRIGLVPFAVLFSVGLILLSRR 59
SSQKHSPVPEKA--IPLITPGSA 86
FNQKPRAPGDEEAQVENLITNAA 87

STANDARD; PRT; 94 AA.
3; Q9CXD0;
Rel. 41, Created
Rel. 41, Last sequence update
Rel. 41, Last annotation update
ontaining ion transport regulator 6 precursor (PLM-like
(Mouse).
cazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
090;
N.A. (ISOFORM 1).
6; TISSUE=Cerebellum;
oba R., Kato K., Matsubara K.;
like ion channel gene expressed in the nervous system.";
3-1999) to the EMBL/GenBank/DBJ databases.

N.A. (ISOFORMS 1 AND 2).
6J; TISSUE=Embryo;
660; PubMed=11217851;
nagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
ara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
awa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
zaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
tsuda H.A., Ashburner M., Batalov S., Casavant T.,
is S., Matsuo Y., Nikaio I., Pesole G., Quackenbush J.,
Schaubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
do T., Furuno M., Aono H., Baldarelli R., Barsh G.,
felli D., Bojunga N., Carninci P., de Bonaldo M.F.,
J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilmi
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN (3)
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=FVB/N; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.I
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz J
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.F
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smallos D.E.,
RA Suterch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9D164-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9D164-2; Sequence=VSP 001585;
CC -!- SIMILARITY: Belongs to the FXVD family.
CC -!- This SWISS-PROT entry is copyright. It is produced through a coll
CC between the Swiss Institute of Bioinformatics and the EMBL out
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB032010; BAB40451.2; --
CC EMBL; AK003888; BAB23058.1; --
CC EMBL; AK018354; BAB31174.1; --
CC EMBL; BC042579; AAH42579.1; --
CC EMBL; BC051127; AAH51127.1; --
CC MGD; MGI:1890226; Fxyd6.
CC InterPro; IPR000272; ATP1G1_PLM_MAT8.
CC Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
CC PROSITE; PS01310; FXVD; 1;
KW Transmembrane; Signal; Ionic channel; Ion transport;
KW Alternative splicing.
FT SIGNAL 1 17
FT CHAIN 18 94
FT FT
FT FT
FT DOMAIN 18 34
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 57
FT DOMAIN 58 94
FT CYTOPLASMIC (POTENTIAL).
FT VARSPLIC 20 20
FT Missing (in isoform 2).
FT /FTid=VSP 001585.
SQ SEQUENCE 94 AA; 10374 MW; 02E22B0BE349CB51 CRC64;
Query Match 26.8%; Score 123.5; DB 1; Length 94;
Best Local Similarity 37.5%; Pred. No. 2.5e-06;
Matches 33; Conservative 15; Mismatches 37; Indels 3; G

OX NCBI_TaxID=3913;
RN {1}
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;

: January 6, 2004, 16:03:17

09:53:14 2004

us-10-063-557-50.rspt

GenCore version 5.1.6
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in search, using sw model

January 6, 2004, 16:00:40 ; Search time 36 Seconds
(without alignments)
637.963 Million cell updates/sec

3-10-063-557-50

1
MERVTLALLLAGLTALEAN.....HSPVPEKAIPITPGSATTC 89

JOSUM62

ipop 10.0 , Gapext 0.5

10525 seqs, 258052604 residues

ts satisfying chosen parameters: 830525

lgth: 0

lgth: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

PTREMBL_23:*

sp archaea:*

sp bacteria:*

sp fungi:*

sp human:*

sp invertebrate:*

sp mammal:*

sp mhc:*

sp organelle:*

sp phage:*

sp plant:*

sp rodent:*

sp virus:*

sp vertebrate:*

sp unclassified:*

sp rvirus:*

sp bacteriophage:*

sp archaea:*

the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

ery	tch	Length	DB	ID	Description

17	66	14.3	446	17	Q97UY7	su
18	65.5	14.2	546	4	Q86NJ9	hom
19	65.5	14.2	582	4	Q8N8P9	hom
20	65.5	14.2	1185	16	Q8EGS8	sh
21	65	14.1	327	10	Q9LVG3	ar
22	65	14.1	469	2	Q9XDX1	mag
23	65	14.1	760	13	Q90638	ga
24	64.5	14.0	155	11	Q9R126	mu
25	64.5	14.0	455	17	Q8TXS5	py
26	64.5	14.0	465	2	O86080	rho
27	64.5	14.0	550	12	Q9QEW9	me
28	64.5	14.0	550	12	Q9QEW7	me
29	64.5	14.0	725	5	Q8SY05	dro
30	64	13.9	315	10	Q9LS88	ar
31	64	13.9	667	5	Q9BJM1	tri
32	64	13.9	678	16	Q8R9G1	th
33	63.5	13.8	309	16	Q92A05	li
34	63.5	13.8	309	16	Q8YSP7	li
35	63.5	13.8	550	12	Q9QEW8	me
36	63.5	13.8	585	6	Q9XSJ8	can
37	63.5	13.8	620	16	O07239	my
38	63.5	13.8	882	10	Q8LSV5	or
39	63	13.7	468	10	Q9ZVA7	ar
40	63	13.7	655	2	Q8KWT9	str
41	63	13.7	655	16	Q8DUN3	st
42	63	13.7	825	12	Q993G5	ca
43	63	13.7	912	16	Q8D4M3	vi
44	63	13.7	923	5	Q9N389	cae
45	63	13.7	1022	5	Q27779	sch

ALIGNMENTS

RESULT 1

ID	Q8BTD2	PRELIMINARY;	PRT;	80 AA.
AC	Q8BTD2;			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	FXD domain-containing ion transport regulator 7.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Body;			
RX	MEDLINE=22354683; PubMed=12466851;			
RA	The FANTOM Consortium,			
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotat			
RT	60,770 full-length cDNAs."			
RL	Nature 420:563-573(2002).			
DR	EMBL; AK004113; BAC35067.1;			
SQ	SEQUENCE 80 AA; 8487 MW; 135CEB39C7A01CDC CRC64;			

Query Match	18.4%;	Score 85;	DB 11;	Length 80;
Best Local Similarity	29.5%;	Pred. NO. 0.04;		
Matches	23;	Conservative	14;	Mismatches 35; Indels 6;
QY	11	LAGTALZANDPPFANKDDPFYVDWKNLQSLGICGLLAIAGIAVLGSKCK-YK		
Db	1	MATTCQSTNVP--EETDPFFDYATVQTGNTLATIMFVLGIILSKVKCKK		
QY	70	HSPVPEKA---IPLITPG 84		
Db	59	BSPTCKSCKSELPSAPG 76		

RESULT 2

Q8IWS1

19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1

RL	Nature 413:523-527(2001).	
DR	EMBL: A3414155; CAC92299.1; --	
DR	Pfam: PF04284; DUF441; L.	
KW	Hypothetical protein; Complete proteome.	
Q	SEQUENCE 150 AA; 15409 MW; E30184B599C5B9B CRC64;	
Query Match 15.0%; Score 69; DB 16; Length 150;		
Best Local Similarity 30.2%; Pred.No.5.4; Mismatches 26; Conservative 14; Indels 14;		
Qy	4 VTIALLLAGLTALEANDPFANKDDPFYDWMKQLSGLICGGLAIAIGI-AAAVI	
Db	26 VTIALLLIAIRITPLNS-----FFPW--VEKYGLTIGVILITIGWVAFIP	
Qy	63 YKSSQKQSPVPEKAIPITPGSATT 88	
Db	73 ISASEVLHSFQWKSILAIIVGVAVS 98	
RESULT 7		
Q8DOY1	ID Q8DOY1 PRELIMINARY; PRT; 157 AA.	
AC	Q8DOY1;	
DT	01-MAR-2003 (TrEMBLrel. 23, Created)	
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)	
DE	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)	
DE	Hypothetical protein.	
GN	V1423.	
OS	Yersinia pestis.	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales	
OC	Enterobacteriaceae; Yersinia.	
NCBI	TaxID=632;	
RP	[1]_TaxID=632;	
RN	SEQUENCE FROM N.A.	
RC	STRAIN=KIMS / Biovar Mediaevalis;	
RX	MEDLINE=22137863; PubMed=12142430;	
RA	Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Li	
RA	Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,	
RA	Petherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,	
RA	Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner	
RA	Ferry R.D.;	
RT	"Genome sequence of Yersinia pestis KIM.";	
RL	J. Bacteriol. 184:4601-4611(2002).	
DR	EMBL: AE013745; AAM84995.1; --	
KW	Hypothetical protein.	
Q	SEQUENCE 157 AA; 16330 MW; A7DBE45E5FFD414F6 CRC64;	
Query Match 15.0%; Score 69; DB 16; Length 157;		
Best Local Similarity 30.2%; Pred.No.5.7; Mismatches 26; Conservative 14; Indels 14;		
Qy	4 VTIALLLAGLTALEANDPFANKDDPFYDWMKQLSGLICGGLAIAIGI-AAAVI	
Db	33 VTIALLLIAIRITPLNS-----FFPW--VEKYGLTIGVILITIGWVAFIP	
Qy	63 YKSSQKQSPVPEKAIPITPGSATT 88	
Db	80 ISASEVLHSFQWKSILAIIVGVAVS 105	
RESULT 8		
Q9LUK8	ID Q9LUK8 PRELIMINARY; PRT; 339 AA.	
AC	Q9LUK8;	
DT	01-OCT-2000 (TrEMBLrel. 15, Created)	
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	
DT	01-OCT-2000 (TrEMBLrel. 15, Last annotation update)	
DE	Phosphate/phosphoenolpyruvate translocator protein-like.	
OS	Arabidopsis thaliana (Mouse-ear cress).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta	
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosi	
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.	
NCBI	TaxID=3702;	

Best Local Similarity 29.0%; Pred. No. 16;					
Matches 20; Conservative 15; Mismatches 21; Indels 13;					
QY	33	DMKNLQLSLG-----ICGGILATAGIAAVLSGCKCYKSQ--KQHSPY			
Dd	270	DWVVLVSALLEADTKLTINLFYGAIAIAGVAAYNNHKLKEASKVVTTETPc			
QY	80	LITPSAATT 88			
Dd	330	LVSQGNNT 338			
RESULT 10					
Q9CL30 PRELIMINARY; PRT; 456 AA.					
ID	Q9CL30				
AC	Q9CL30;				
DC	01-JUN-2001 (TReMBLrel. 17, Created)				
DT	01-JUN-2001 (TReMBLrel. 17, Last sequence update)				
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)				
DE	Hypothetical protein PM1417.				
DN	PM1417.				
GE	Pasteurella multocida.				
OS	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;				
OC	Pasteurellaceae; Pasteurella.				
OX	NCBI_TaxID=747;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN:Pm70;				
RX	MEDLINE=21145866; PubMed=11248100;				
RT	May B.-J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur				
RT	"Complete genomic sequence of Pasteurella multocida Pm70.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).				
DR	EMBL; AE006178; AAK03501.1; -				
DR	InterPro: IPR001807; Cl-channel_volt.				
DR	Pfam: PF00654; voltage_CLC; 1.				
DR	PRINTS; PROU762; CLCHANNEL.				
KW	Hypothetical protein; Complete proteome.				
SQ	SEQUENCE 456 AA; 49349 MW; AA9C46DBD68D4ED0A CRC64;				
Query Match 14.9%; Score 68.5; DB 16; Length 456;					
Best Local Similarity 29.7%; Pred. No. 22;					
Matches 22; Conservative 14; Mismatches 23; Indels 15;					
QY	2	ERVTLALLLAG--ITALLEANDPF-----ANKDDPPFYDWKNLQLSGLIC---G			
Dd	211	ERRVLGLVLAAGFILVAIEGNNPVFPQHGTSVPYLFLW--VSLGVVCVGFPG			
QY	50	-IAG-AAVLSGCKC 62			
Dd	269	LVKGLAGLSPSKIR 282			
RESULT 11					
Q8HKR3 PRELIMINARY; PRT; 173 AA.					
ID	Q8HKR3				
AC	Q8HKR3;				
DC	01-MAR-2003 (TReMBLrel. 23, Created)				
DT	01-MAR-2003 (TReMBLrel. 23, Last sequence update)				
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)				
DE	NADH dehydrogenase subunit 6.				
DN	ND6.				
OS	Arcos sp. KU-149.				
OC	Mitochondrion.				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;				
OC	Acanthopterygii; Acanthopterygii; Perciformes;				
OC	Gobiiesocidae; Gobiiesocidae; Arcos.				
OX	NCBI_TaxID=181474;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Muscle;				
RA	Miya M.;				
RA	Submitted (DSC-2001) to the EMBL/GenBank/DBI databases				

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4 N.A.
3;
Shima H., Endo H., Ishiguro N.B., Inoue J.G., Mukai T.,
(amaguchi M., Kawaguchi A., Mabuchi K., Shirai S.M.,
ns of higher teleostean phylogenies: A new perspective
complete mitochondrial DNA sequences.";
et. Evol., 26:121-138(2002).
52; BAC23785.1; -.
1.
13 AA; 17892 MW; 5FF3D10C1CBF8A2A CRC64;
    14.8%; Score 68; DB 8; Length 173;
arity 30.2%; Pred.No.8.3;
onservative 14; Mismatches 28; Indels 2; Gaps 2;
ALLAGLTALBANDPFANKDDPFYDWKQLQSLGILCGLLAIAGIAAVLSGCKY 63
LIVLGMLVVPAYSA-ALAAEPYPETWGSPLVLGLMCGYLGVGLGVVSFWGMY Y 110
66
113
RELIMINARY; PRT; 664 AA.
TREMBLrel. 08, Created)
TREMBLrel. 08, Last sequence update)
TREMBLrel. 23, Last annotation update)
brane spanning receptor TRC8 (Patched related protein
(Human).
tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Primates; Catarrhini; Homnidae; Homo.
106;
1 N.A.
1199; PubMed=9689122;
West J.D.; Boldog F., Tanaka N., Robinson L.J.,
ri F., Drablin H.A.;
ry renal cell carcinoma 3; 8 translocation fuses PHIT to a
ed gene, TRC8.";
cad. Sci. U.S.A. 95:9572-9577(1998) .
Y: CONTAINS 1 RING-TYPE ZINC FINGER.
1; AAC39930.1; -
10; AAC39931.1; -
1001841, ZnF_ring.
; ZF-C3HC4; 1.
14; RING; 1.
1089; ZF_RING_2; 1.
; Zinc; Zinc-finger.
4 AA; 76007 MW; 55EB6C925B5ED4D3 CRC64;
    14.6%; Score 67.5; DB 4; Length 664;
arity 28.6%; Pred.No.43;
onservative 11; Mismatches 24; Indels 15; Gaps 3;
TLALLIAGLTALBANDPFANKDDPFYDWK-----NLQSLGILCGLLAIAGI 53
TAQTATVMYLRM-----ANETSFFISWDDFWLICNLIISG--CDSTLTVLGM 294
SGCKY 63
| |
:SSVAHY 304

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ID QWU17 PRELIMINARY; PRT; 664 AA.
AC QWU17;
DC 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Patched related protein translocated in renal cancer.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR ENBL; BC021571; AAH21571.1; -.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4.1.
DR SMART; SM00184; RING.1.
DR PROSITE; PS0089; ZF_RING.2; 1.
DR Metal-binding; Zinc; Zinc-finger.
KW SEQUENCE 664 AA; 75993 MW; 9885F5915F019EF5 CRC64;
SQ
Query Match 14.6%; Score 67.5; DB 4; Length 664;
Best Local Similarity 28.6%; Pred.No. 43;
Matches 20; Conservative 11; Mismatches 24; Indels 15;
QY 1 MERVTLALLAGLTALANDPFANKDDPFYDQK-----NLQSLGLICGLL
Db 243 LIRVTAQATVLMYLRM-----ANETSPFISWDDFMDLNLIISS--CDSTL
QY 54 AAVALSGCKCY 63
Db 295 SAVISSVAHY 304
RESULT 14
Q9K313 PRELIMINARY; PRT; 241 AA.
ID Q9K313;
AC Q9K313;
DC 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative ABC transport system integral membrane protein.
GN SC01257 OR 2SGC18.04c.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bactman A., Brown S., Chandra G., Chen C.W., Collins I.
RA Cronin A., Fraser A., Goble A., Hidalgo J., Howarth I.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor
RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RL "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR ENBL; AL939108; CAB99137.1; -.
KW Complete proteome.
SQ SEQUENCE 241 AA; 24559 MW; 300F70FACD254926 CRC64;
Query Match 14.4%; Score 66.5; DB 16; Length 241;
Best Local Similarity 28.4%; Pred.No. 18;
Matches 27; Conservative 15; Mismatches 32; Indels 21;

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ALLLLAGLTALEANDPFANKDDPFFYDWKNLOLSGLICGGLIAIAGIAAVLSGKCKY 63
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
AFSALAG-----SSDASAPDFDLF-----TALSVMFGQIAAIAFGALVVSSEYQG 79
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
KQKHSVPPEK-----AIPLITPGSAT 87
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
RLSLAAVPQGRWFAAKLAVIAPLVVLAT 114
PRELIMINARY; PRT; 516 AA.

(TEMBLrel. 01, Created)
(TREMBLrel. 08, Last sequence update)
(TREMBLrel. 22, Last annotation update)
e-sensitive voltage-gated potassium channel.

cuniculus (Rabbit).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Lagonomorpha; Leporidae; Cryptologus.
986;

M N A.
ealand White;
9424; PubMed=8647945;
g A.Y., Boulpaep E.L., Segal A.S., Desir G.V.;
loning of a glioblastamide-sensitive, voltage-gated
annel expressed in rabbit kidney." ;
est. 97:2525-2533(1996).
; AAC24719.1 ; -.
; R000210; BTB_POZ.
R005821; Ion_trans.
R001622; K+channel_pore.
R004050; Kv3channel.
R003968; Kv_channel.
R003091; K_channel.
R003131; K_tetra.
R005820; M+channel_nlg.
R003972; Shaker_channel.
O; ion_trans; 1.
4; K_tetra; 1.
169; KOCHANNEL.
510; KV13CHANNEL.
491; KVCHANNEL.
496; SHAKERCHANNEL.
25; BTB; 1.
1; Transmembrane.
16 AA; 57430 MW; 795E84998BCATCAA CRC64;

14.4%; Score 66.5; DB 6; Length 516;
larity 20.1%; Pred.NO.42;
Conservative 14; Mismatches 36; Indels 69; Gaps

LAGLTALENDP---FANKDDPF-----YYDWKNLOLSLICGGLIATAGI 53
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
SSAVIFYAEADDPSTSGFSSIPDAFWAAVVTMTTVGYGDHPVTIGGKVGSILCAIAGV 41
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
'L-----SGKKYKSSQKQ-----69
ALPVPVSNFNFYHRETGEESQAQMVGSCQHLLSSSAELRKARNSTLSKSEY 470
-----HSPVPEKAIPLITPGSATTC 89
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
BEGMNHSAPFQ--TPFKTNSTATC 497
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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January 6, 2004, 16:04:06

XX
KW Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's diseases; ovulatory defect;
KW muscular dystrophy.
XX
OS Homo sapiens.
XX
PN WO200000610-A2.
XX
PD 06-JAN-2000.
XX
PF 25-JUN-1999; 99WO-US14484.
XX
PR 26-JUN-1998; 98US-0090762.
PR 31-JUL-1998; 98US-0094983.
PR 01-OCT-1998; 98US-0102686.
PR 11-DEC-1998; 98US-0112129.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
DR WPI; 2000-160673/14.
DR N-PSDB; AAZ98143.
XX
PT New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and
PT cardiovascular disease -
XX
PS Claim 1; Page 182; 327pp; English.
XX
CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
CC neuroprotective, cardiovascular and antiasthmatic activities, and can
CC be used in gene therapy. HSPPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSPP. Antagonists of
CC HSPP are used to treat or prevent disorders associated with increased
CC activity or function of HSPP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
CC nucleic acids can be used for the recombinant production of HSPP, for
CC detecting HSPP in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense,
CC triplex-forming or ribozyme therapeutics, for detecting related sequences
CC or genetic variations, and for chromosomal mapping. HSPP are also used to
CC raise specific antibodies (Ab) and to screen for agonists and
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
CC monitor, HSPP-related diseases (in usual immunoassays), as therapeutic
CC antagonists, in competitive drug screens, and for purification of HSPP
CC from natural sources.
XX
SQ Sequence 89 AA;

Query Match 100.0%; Score 461; DB 21; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e-50;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERVTLALLLLAGLTALEANDPFANKDDPFYDWNKQLQSLICGGLLAIAGIAAVLSGK 60
Db 1 MERVTLALLLLAGLTALEANDPFANKDDPFYDWNKQLQSLICGGLLAIAGIAAVLSGK 60

QY 61 CKYKSSQKQHSVPVEKAIPILITPGSATTC 89
Db 61 CKYKSSQKQHSVPVEKAIPILITPGSATTC 89